

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		Result No.	Score	% Query Match	Length	DB	ID	Description	
Run on:	November 27, 2003, 11:04:55 ; Search time 1982 Seconds	1	311	96.3	830	8	MZPCSSU	D00170 Zea mays mRNA	
	66666.907 Million cell updates/sec	2	311	96.3	830	8	ZMRBSSU	MZPCSSU Maize rRNA	
Title:	US-09-987-899-5	3	295	91.3	1648	8	ZMRBCS	Y00322 Maize rbcS	
Perfect score:	323	4	271	83.9	1274	8	ZMRBMSU	Y09214 Z.mays rbcS	
Sequence:	1 cgaccgtgctgaaggatgg.....ccggccccggccccc 323	5	222.6	68.9	2328	8	SCEFBCL	Y096717 Saccharum h	
Scoring table:	IDENTITY_NUC	6	201.8	62.5	808	8	RICCRBCL	I22155 Oryza sativ	
	Gapop 10^-0 , Gapext 1.0	7	201.8	62.5	830	8	RICRBPC1	D00643 Oryza sativ	
Searched:	2888711 seqs, 20454813386 residues	8	201.8	62.5	145880	8	CNE08C70	ALI731739 Oryza sat	
Total number of hits satisfying chosen parameters:	5777422	9	198.8	61.5	960	6	B069808	E069808 Zoysia rbs	
Minimum DB seq length: 0		10	198.6	61.5	854	8	AF017364	AF017364 Oryza sat	
Maximum DB seq length: 20000000000		11	197	61.0	835	8	AF052305	AF052305 Oryza sat	
Post-processing: Minimum Match 0%		12	192.2	59.5	591	8	AB010942	Secale ce	
	Total number of hits satisfying chosen parameters:	13	192.2	59.5	604	8	AB020944	Agropyron	
Minimum DB seq length: 0		14	192.2	59.5	787	8	AB020954	AB020954 Triticum	
Maximum DB seq length: 20000000000		15	192.2	59.5	895	8	RICRBPC2	D0042065 Oryza sativ	
Post-processing: Minimum Match 0%		16	190.6	59.0	638	8	AB042065	AB042065 Triticum	
	Total number of hits satisfying chosen parameters:	17	190.6	59.0	781	8	AB020953	AB020953 Aegilops	
Minimum DB seq length: 0		18	190.6	59.0	787	8	AB020955	AB020955 Triticum	
Maximum DB seq length: 20000000000		19	190.6	59.0	127767	2	CNS09S4U	BX119951 Oryza sat	
Post-processing: Maximum Match 10%		c	20	189.6	58.7	845	8	SCF131737	AF131737 Secale ce
	Listing first 45 summaries	21	189	58.5	504	8	AF192776	AF192776 Avena cla	
Database :	GenBank:	22	189	58.5	504	8	AF192779	AF192779 Avena mar	
	1: gb_ba:*	23	189	58.5	605	8	AB020943	AF019276 Avena mar	
	2: gb_htg:*	24	189	58.5	611	8	AB020937	AB020937 Aegilops	
	3: gb_in:*	25	189	58.5	781	8	AB020958	AB020958 Triticum	
	4: gb_om:*	26	189	58.5	2205	8	WTRUBIAA	M27328 T. aestivum	
	5: gb_ov:*	27	189	58.5	5980	8	AB042069	AB042069 Triticum	
	6: gb_pat:*	28	188	58.2	789	8	AB020959	Secale ce	
	7: gb_ph:*	29	187.4	58.0	600	8	AF020645	AB020959 Avena cla	
	8: gb_Pl:*	30	187.4	58.0	604	8	AB020939	AB020939 Triticum	
	9: gb_pr:*	31	187.4	58.0	607	8	AB020938	AB020938 Aegilops	
	10: gb_rc:*	32	187.4	58.0	611	8	TARUBL	X00234 Wheat mRNA	
	11: gb_sts:*	33	187.4	58.0	728	8	AB020952	AB020952 Aegilops	
	12: gb_sy:*	34	187.4	58.0	792	8	AB020949	AB020949 Aegilops	
	13: gb_un:*	35	187.4	58.0	792	8	AB020950	AB020950 Aegilops	
	14: gb_v1:*	36	187.4	58.0	985	8	AB042068	AB042068 Triticum	
	15: em_ba:*	37	185.8	57.5	504	8	AF192773	AF192773 Avena aga	
	16: em_fun:*	38	185.8	57.5	605	8	AB020932	AB020932 Aegilops	
	17: em_hum:*	39	185.8	57.5	605	8	AB010933	AB010933 Aegilops	
	18: em_in:*	40	185.8	57.5	605	8	AB020934	AB020934 Aegilops	
	19: em_mu:*	41	185.8	57.5	605	8	AB020935	AB020935 Aegilops	
	20: em_om:*	42	185.8	57.5	605	8	AB020936	AB020936 Aegilops	
	21: em_or:*	43	185.8	57.5	620	8	AF202648	AF202648 Avena mar	
	22: em_cv:*	44	185.8	57.5	787	8	AB020946	AB020946 Aegilops	
	23: em_pat:*	45	185.8	57.5	875	8	CSE131738	AF131738 Secale ce	
	24: em_ph:*								
	25: em_Pl:*								
	26: em_ro:*								
	27: em_sts:*								
	28: em_un:*								
	29: em_v1:*								
	30: em_htg_hum:*								
	31: em_htg_inv:*								
	32: em_htg_other:*								
	33: em_htg_mus:*								
	34: em_htg_pln:*								
	35: em_htg_rod:*								
	36: em_htg_man:*								
	37: em_htg_vrt:*								
	38: em_sy:*								
	39: em_htgo_hum:*								
	40: em_htgo_mus:*								
	41: em_htgo_other:*								

Pred. No. is the number of results predicted by chance to have a 1 (bases 1 to 830)

RESULT 1
 MZPCSSU LOCUS
 Zea mays mRNA for ribulose 1,5-bisphosphate carboxylase small subunit, complete cds.
 DEFINITION
 ACCESSION D00170
 VERSION D00170.1 GI:217963
 KEYWORDS RubBC; ribulose-1,5-bisphosphate carboxylase; small subunit.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE MatsuoKA,M., Kano-Murakami,Y., Tanaka,Y., Ozeki,Y. and Yamamoto,N.

TITLE	Nucleotide sequence of cDNA encoding the small subunit of ribulose-1,5-bisphosphate carboxylase from maize													
JOURNAL	J. Biochem. 102 (4), 673-676 (1987)													
MEDLINE	81139216													
PUBMED	3436948													
COMMENT	Comparison with the RuBPC small subunit genes from other plants revealed that the maize small subunit is similar to the wheat one, there being 73% homology between the transit peptides and 64% noteworthy difference between the C3 and C4 small subunit structures.													
FEATURES	Location/Qualifiers													
source	1..830	/organism="Zea mays"												
CDS	/product="ribulose-1,5-bisphosphate carboxylase small subunit"	/mol_type="mRNA"												
	/db_xref="GR:217964"	/db_xref="taxon:4577"												
	/tissue_type="leaf"	66..578	/codon_start=1											
	/note="SSU"	/product="ribulose-1,5-bisphosphate carboxylase (RuBPC)"	/product="ribulose-1,5-bisphosphate carboxylase (RuBPC)"											
	/odon_start=1	/protein_id="CAA29784.1"	/protein_id="CAA29784.1"											
	/product="ribulose-1,5-bisphosphate carboxylase small1"	/db_xref="GI:12474"	/db_xref="P05348"											
	/mol_type="mRNA"	/mol_type="mRNA"	/t_translation="MAPTVNMASSATAVAPFQGLKSTASLPPVARRSSRLGNVSNNGRIRCMQWPAVGNKKPETLSLPLSTDDILKQDYLRLNGWICLFLPSKVGFYRENSTPCYDGRYWTWKLPNGCNDATQVYRELQEAISYPDAFHRYVIGFDNIKIQCVSFIAYKPGSD"											
BASE COUNT	147 a	281 c	220 g	182 t										
ORIGIN					BASE COUNT	147	a	281	c	220				
					ORIGIN					t				
Query Match	96.3%	Score 311;	DB 8;	Length 830;	Query Match	96.3%	Score 311;	DB 8;	Length 830;	Query Match	96.3%	Score 311;	DB 8;	Length 830;
Best Local Similarity	99.7%	Pred. No. 2..3e-48;	Indels 0;	Mismatches 0;	Best Local Similarity	99.7%	Pred. No. 2..3e-48;	Indels 0;	Mismatches 0;	Best Local Similarity	99.7%	Pred. No. 2..3e-48;	Indels 0;	Mismatches 0;
Matches	322	Conservative	0;	Gaps 1;	Matches	322	Conservative	0;	Gaps 1;	Matches	322	Conservative	0;	Gaps 1;
Qy	1	CGACCTGCTGAAGCAGGTGACTACCTGCTGATACCCCTGCCTCGAGTT	60		Qy	1	CGACCTGCTGAAGCAGGTGACTACCTGCTGCTGCAACGGCTGATCCAGTT	60		Qy	1	CGACCTGCTGAAGCAGGTGACTACCTGCTGCTGCAACGGCTGATCCAGTT	60	
Db	278	CGACCTGCTGAAGCAGGTGACTACCTGCTGCAACGGCTGATCCCTGCTCGAGTT	337		Db	278	CGACCTGCTGAAGCAGGTGACTACCTGCTGCTGCAACGGCTGATCCAGTT	337		Db	278	CGACCTGCTGAAGCAGGTGACTACCTGCTGCTGCAACGGCTGATCCAGTT	337	
Qy	61	CAGGAGGTGGCTTCGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGGCG	120		Qy	61	CAGGAGGTGGCTTCGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGCCG	120		Qy	61	CAGGAGGTGGCTTCGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGCCG	120	
Db	338	CAGGAAAGGTGGCTGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGCCG	397		Db	338	CAGGAAAGGTGGCTGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGCCG	397		Db	338	CAGGAAAGGTGGCTGTTGAGTACCCGGAGAACTCCACCTCCGGTACTACGAGGCCG	397	
Qy	121	CTACTGGACATCTGGAGCATGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	180		Qy	121	CTACTGGACATCTGGAGCATGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	180		Qy	121	CTACTGGACATCTGGAGCATGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	180	
Db	398	CTACTGGACATCTGGAGAACCTGGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	456		Db	398	CTACTGGACATCTGGAGAACCTGGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	456		Db	398	CTACTGGACATCTGGAGAACCTGGCCATGAGCATGCCATTCGGCTGAGAAGCTACA	456	
Qy	181	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	240		Qy	181	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	240		Qy	181	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	240	
Db	457	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	516		Db	457	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	516		Db	457	AGGAGCTGGAGGAGCCATCAAATCCTAACCGGAGCCCTTCCACCGGCTCATGGCTTCG	516	
Qy	241	ACAAACATCAAGAGCAGCTGAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	300		Qy	241	ACAAACATCAAGAGCAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	300		Qy	241	ACAAACATCAAGAGCAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	300	
Db	517	ACAAACATCAAGAGCAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	576		Db	517	ACAAACATCAAGAGCAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	576		Db	517	ACAAACATCAAGAGCAGCTGAGTGGCTCATGGCTTACAGCCCCGGGAGCCACT	576	
Qy	301	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	323		Qy	301	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	323		Qy	301	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	323	
Db	577	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	599		Db	577	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	599		Db	577	AGACGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC	599	
RESULT 2	ZMRBUSSU	830 bp	mRNA	linear	RESULT 3	ZMRBCS	1648 bp	DNA	linear	RESULT 3	ZMRBCS	1648 bp	DNA	linear
DEFINITION	Maize mRNA for ribulose-1,5-bisphosphate carboxylase small subunit				DEFINITION	Maize rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit				DEFINITION	Maize rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit			
ACCESSION	X06535				ACCESSION	Y00322				ACCESSION	Y00322			
VERSION	X06535.1				VERSION	Y00322.1				VERSION	Y00322.1			
KEYWORDS	ribulose bisphosphate carboxylase; transit peptide				KEYWORDS	ribcS gene; ribulose bisphosphate carboxylase.				KEYWORDS	ribcS gene; ribulose bisphosphate carboxylase.			
SOURCE	Zea mays				SOURCE	Zea mays				SOURCE	Zea mays			
ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD				ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			

REFERENCE	1 (bases 1 to 1648)	Db	1102 ACAACATCAAGCAGAACGGAGTGTGCTCATGCCCTACAGCCCGGGGAGCGACT 1161
AUTHORS	Lebrun, M., Wakeman, G. and Freysinet, G.	Qy	301 AGACCGCSCCGGCC 323
TITLE	Nucleotide sequence of a gene encoding corn ribulose-5'-bisphosphate carboxylase/oxygenase small subunit (rbcs)	Db	1162 AGACCGCSCCGGCC 1184
JOURNAL	Nucleic Acids Res. 15 (10), 4360 (1987)		RESULT 4
MEDLINE	87231019	ZMRUBMSU	ZMRUBMSU
PUBMED	3588298	LOCUS	1274 bp
AUTHORS	2 (bases 1 to 1648)	DEFINITION	Z.mays rubisco small subunit gene.
ARTISTS	Freysinet, G.	ACCESSION	Z.mays Y09214
TITLE	Direct Submission	VERSION	Y09214.1 GI:1673455
JOURNAL	Submitted (16-OCT-1987)	KEYWORDS	rubisco small subunit.
FEATURES	Location/Qualifiers	SOURCE	zea mays
source	1..1648	ORGANISM	Zea mays
	/organism="Zea mays"	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	/mol_type='genomic DNA'	AUTHORS	spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
	/strain="F2"	JOURNAL	clade; Panicoideae; Andropogoneae; Zea.
	/db_xref="taxon:4577"	REFERENCE	1
CNAT_signal	359..362	AUTHORS	Ewing, R.M.
TATA_signal	398..403	JOURNAL	Thesis (1996) Department of Plant Sciences, University of Oxford, U.K.
gene	join(491..637,801..1163)	REFERENCE	2 (bases 1 to 1274)
	/gene=rbcs	AUTHORS	Ewing, R.M.
	join(491..637,801..1163)	JOURNAL	Direct Submission
	/gene=rbcs	TITLE	Submitted (05-NOV-1996) R.M. Ewing, University of Oxford, Plant Sciences, South Parks Road, Oxford, OX1 3RB, UK
	/EC_number="4.1.1.39"	FEATURES	Location/Qualifiers
	/codon_start=1	1..1274	
	/product="ribulose 1,5-bisphosphate carboxylase/oxygenase"	/organism="Zea mays"	
	/protein_id="CA68419..1"	/mol_type="genomic DNA"	
	/db_xref="GI: 22465"	/db_xref="taxon: 4577"	
	/db_xref="SWISS-PROT: P05348"	/chromosome="21"	
	/translation="MAPTVMASSATAAVAPFQGLKSTASLPEVARSSRSLSQNVNSNGR	/cell_line="b73"	
	IRCMQWMPAYNMKFWKLPMFGCNDAQTVYKELQAIKSYPDFNKRVIDPDKNIQTQCVSF	join(196..342..461..826)	
	IAKYKPPGSID"	/codon_start=1	
	491..637	/product="ribisco small subunit"	
	/gene="rbcs"	/protein_id="CA70416..1"	
	/number=1	/db_xref="GI: 1673455"	
misc_feature	631..632	/db_xref="SPREMBL:O44574"	
	/gene="rbcs"	/translation="MAPTMMASSATAAVAPFQGLKSAASLPVARRSTRSLGNVNSNGR	
	/note="pot. site of cleavage of transit peptide"	IRCMQWMPAYNMKFWKLPMFGCNDAQTVYKELQAIKSYPDFNKRVIDPDKNIQTQCVSF	
	638..800	TSPCYDGRWTTWWKLPMPFGCDTQVYKELQEAAYDPDHRVIGFDNVRTQCVS	
	/gene="rbcs"	FLAYKPGSE"	
	/number=1	<196..342	
intron	801..1160	/number=1	
	/gene="rbcs"	343..460	
	/number=2	/number=1	
	exon	461..826	
	368 a	/number=2	
BASE COUNT	509 c	exon	
ORIGIN	360 t	intron	
		exon	
		BASE COUNT	279 a
		ORIGIN	397 c
			310 g
			288 t
Query Match	91.3%	Score 295;	Length 1648;
Best Local Similarity	98.8%	DB 8;	
Matches	319; Conservative	Mismatches 0;	
		Indels 4;	
		Gaps 2;	
Qy	1 CGACCTGTGAAAGCAGGTGACTACTCTGCTGGATAACGGCTGGT 60	Query Match	83.9%
	CGACCTGTGAAAGCAGGTGACTAC - - CTGCGCAACCGCTGGT 922	Best Local Similarity	92.0%
Db	866 CAGCAAGTCGGTTCGGTACGGGAGAAGTCACTCCCGTGTACTAACCGCCCG 120	Matches	297; Conservative
Qy	61 CAGCAAGTCGGTTCGGTACGGGAGAAGTCACTCCCGTGTACTAACCGCCCG 982	0; Mismatches 25;	
Db	923 CAGCAAGTCGGTTCGGTACGGGAGAAGTCACTCCCGTGTACTAACCGCCCG 180	Indels 1; Gaps 1;	
Qy	121 CTAAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 1041	Qy	1 CGAACCTGTGAAAGCATGCCATGGTGGCTGCAACAGCCACGGCTGCTGAGTT 60
Db	983 CTAAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 1101	Db	526 CGAACCTGTGAAAGCATGCCATGGTGGCTGCAACAGCCACGGCTGCTGAGTT 585
Qy	181 AGAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 240	Qy	121 CTAAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 180
Db	1042 AGAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 240	Db	646 CTAAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 704
Qy	241 AGACATGAAGAGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 300	Qy	181 AGAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 240
Db	705 AGAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 764	Db	705 AGAGCTGCAGGAGCCATCAATCTAACCGGAGCCTCACGGCT 764

RESULT 5
SCBCCSIA SCBCCS1A 2328 bp DNA linear PLN 16-JUN-1999
DEFINITION Saccharum hybrid cultivar H32-8560 ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit gene, complete cds.
ACCESSION M86717
VERSION M86717.1 GI:169841
KEYWORDS Saccharum hybrid cultivar H32-8560
ORGANISM Saccharum hybrid cultivar H32-8560
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 2328)
AUTHORS Tang, W. and Sun, S.S.
TITLE Sequence of a sugarcane ribulose-1,5-bisphosphate
carboxylase/oxygenase small subunit gene
JOURNAL Plant Mol. Biol. 21 (5), 949-951 (1993)
MEDLINE 93222494
PUBLISHED 8467089

FEATURES source
1. 2328 /organism="Saccharum hybrid cultivar H32-8560"
/mol_type="genomic DNA"
/cultivar="H32-8560"
/db_xref="taxon:50502"
1.066 .. 1071
join(1172, 1315..1411, .1773)
/rnote="ORF"
/codon_start=1
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small subunit"
/protein_id="AAA33922_1"
/cb_xref="GI:169842"
/translation="MAITUMMASATAAAPFQKSTASLIVAPPMTTSIYAKVNSNGRI
RCNQWPAVNPKFETULPKLQDYLURNNWPCLFSKEGVYRENST
SPCYDGRYIWKLPMFGCTASQVYKELQEAIASYPFLRALLGFDNIROTQWLFIF
AVKPGASE"
1172 .. 1309
join(1310, 1315..1411, .1770)
/product="ribulose 1,5-bisphosphate carboxylase/oxygenase
small subunit"
exon 1172 .. 1315
/number=1
1316 .. 1410
/number=1
1411 .. >number=2
CDS
BASE COUNT 539 a 679 c 578 g 532 t
ORIGIN polyA_site 808
Query Match 68.9%; Score 222.6; DB 8; Length 2328;
Best Local Similarity 87.5%; Pred. No. 6..3e-32; Indels 4; Gaps 2;
Matches 267; Conservative 0; Mismatches 34;

Qy 241 ACACATCAAGCAGACCGAGTGGTCAGCTTCATCGCCTAACAGCCGAGGACT 300
Db 765 AGACGTCAGGAGACCGAGTGGTCAGCTTCATCGCCTAACAGCCGAGGACT 824
Qy 301 AGACGCCCGCCGGCCCC 323
Db 825 AGAACCTGGTAGATGACCC 847

Qy 123 ACTGGACCATGGGAGCATGCCATGTTGGCTGAACCAAGGCCACCCAGGTACAAG 182
Db 1598 ACTGGACCATGGGAGCATGCCATGTTGGCTGAACCAAGGCCACCCAGGTACAAG 1656
Qy 183 GAGCTCAGGAGGCCATCAATCTAACCGGACGCCCTCCAGCTGAC 242
Db 1657 GAGCTCAGGAGGCCATCCGGCTAACCGGACGCCCTCCAGCTGAC 1713
Qy 243 AACATTAAGGAGACCGAGTGGTCAGCTAACAGCCGAGGACTAG 302
Db 1714 AACATTAAGGAGACCGAGTGGTCAGCTAACAGCCGAGGACTAG 1773

RESULT 6
SCBCCBCLIA RICCPBBLIA 808 bp mRNA linear PLN 21-DEC-1995
DEFINITION ORyza sativum mitochondrial ribulose bisphosphate carboxylase/oxygenase (rbcS) mRNA, complete Cds
ACCESSION L22155
VERSION L22155..1 GI:347450
KEYWORDS ribulose bisphosphate carboxylase/oxygenase.
SOURCE chloroplast Oryza sativa
ORGANISM Oryza Sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzeae; Oryzae.
REFERENCE 1 (bases 1 to 808)
AUTHORS Moon, E.P., Lee, K.W., Lee, J.S., Choi, Y.D. and Kim, H.J.
TITLE Isolation and Characterization of cDNAs for Ribulose Bisphosphate Carboxylase Multigene Family in Rice (Oryza)
JOURNAL Mol. Cells 1, 287-294 (1991)
COMMENT Original source text: Chloroplast Oryza sativa leaf etiolated cDNA to mRNA. Location/Qualifiers
FEATURES source
1. 808 /organism="Oryza sativa"
/organanelle="plastid;chloroplast"
/mol_type="mRNA"
/db_xref="NCBI:347451"
/tissue="leaf"
/dev_stage="1 .. 808"
/gene="rbcS"
/cds
/gene="rbcS"
/function="incorporate carbon dioxide to ribulose 1,5
bisphosphate"
/note="parative"
/codon_start=1
/product="ribulose 1,5-bisphosphate carboxylase"
/protein_id="AA84592_1"
/db_xref="NCBI:347451"
/translation="MASSATTAVPAPQGLKSTAGMPVARSNSSFGNVNSNGRIRCMQV
WPIEGIKKFETLSVYLPPLTVEILKQIEYLRSKHPVPCFKLPSKEGVYRENST
DGRYNTMMWKLPMFEGCTDATQVLKELEAKAYPDAFVRITGFDNTRVQLQJSLFIAYK
PGCEBGGN"

Qy 2 GACCTGCTGAAGCAGCTTCTGTCAGCGGAGAACCTCCCGTGTCTGACTCTGCTGAGTC 61
Db 1478 AGCTGTGAGCAGCTTCTGTCAGCGGAGAACCTCCCGTGTCTGACTCTGCTGAGTC 1537
Qy 63 GCAAGGTGCGCTTCTGTCAGCGGAGAACCTCCCGTGTCTGACTCTGCTGAGTC 122
Db 1538 GCAAGGAAGGCGCTTCTGTCAGCGGAGAACCTCCCGTGTCTGACTCTGCTGAGTC 1597

BASE COUNT 40123 a /clone lib="OS7NBA" 31371 c 33174 g 40721 t 1 others

ORIGIN Query Match 62.5%; Score 201.8; DB 8; Length 145890; Pred. No. 3.3e-28; Best Local Similarity 81.0%; Mismatches 0; Indels 1; Gaps 1; Matches 247; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

Qy 2 GACCTCTGAGGAGGTGGATACCTGCTGGCAAGGGCTGATACCTGCCTCGAGTTC 61

Db 532 GACCTCTCAGCAGTCAACTGATCCAACTGGCTGCCTCGAGTTC 591

Qy 62 AGCAAAGGTCGGCTTCCTGTACCGCGGAAGCTCCCTGGTACTAGACGCCGC 121

Db 592 AGCAAGGTCGGCTTCCTGTACCGCGGAAGCTCCCTGGTACTAGACGCCGC 651

Qy 122 TACTGGACCATGTGGAGAGCATGCCCATGTTGGTCCAGTGTTGACAA 181

Db 652 TACTGGACCATGTGGAGAGCATGCCCATGTTGGTCCAGTGTTGACAA 710

Db 82591 AGCAAGGTCGGCTTCGCTACCGCGAGAACCTCCCTGGTACTAGACGCCGC 121

Qy 182 GGAGCTCAGGGGGTGGATTGTACCCGTGAGAACCAAGATCCCCGGATACTGGAGG 82656

Db 711 GGAGATGGAGGTGGAAAGGGGGCTAACCCGACTCATCGGGTCA 770

Db 82657 TACTGGACCATGTGGAAAGC-TGCCCATCTCGGGTGCAGTCAGGTGCTCA 82715

Qy 242 CAACATCAAGAGAGCGAGTCGTCGCTCATGGCTTAAGAGCCCAGGCAACTA 301

Db 771 CAACTCAGGAGGGTGGAGGTCAGGTCATGGCTCATGGCTTAAGAGCCCAGGCAACTA 830

Db 82776 GGAGCTCAGGGGGCCAGAGGGGTGACCTGTGCTCATGGCTTAAGAGCCCAGGCAACTA 82775

Qy 302 GACCGGGCCC 311

Db 831 ACCGCAACTC 840

RESULT 10 AF017364 mRNA linear PLN 18-SEP-1997

LOCUS AF017364 mRNA, complete cds.

DEFINITION Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit

ACCESSION AF017364

VERSION AF017364.1 GI:2407282

KEYWORDS

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 854)

AUTHORS Lee, M.C., Kim, C.S. and Eun, M.Y.

TITLE Characterization of Ribulose 1,5-bisphosphate carboxylase small subunit from rice

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 854)

AUTHORS Lee, M.C., Kim, C.S. and Eun, M.Y.

JOURNAL Direct Submission

COMMENT Submitted (07-AUG-1997) Cytogenetics, International Institute of Agricultural Science and Technology, Sedun-Dong, RDA, Suwon 441-707, Korea

FEATURES source

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/strain="Milyang 23"

/db_xref="KCDM2416"

/dev_stage="immature seed (milky stage)"

/product="ribulose 1,5-bisphosphate carboxylase small subunit"

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/db_xref="ISI:2407283"

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BASE COUNT 173 a 239 c 230 g 212 t

ORIGIN

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FEATURES

Source 1. .960

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/db_xref="taxon:22644"

BASE COUNT 201 a -285 c 273 g 201 t

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BASE COUNT	119 a	178 c	165 g	129 t					
ORIGIN									
Query Match	59.5%	Score 192.2;	DB 8;	Length 591;					
Best Local Matches	80.1%;	Prd. No. 3..3e-26;							
Matches	238;	Conservative	0;	Mismatches 58;	Indels 1;	Gaps 1;			
Qy	2	GACCTGGTAAAGAGGTGGACTACCTGTTGGCAACCGCTGATAACCTGGCTCGAATTTC	61						
Db	293	GCCCTCTGAAAGCAGGTGGACTCATCGTCAAGTGTTAACCTGGCTCGAATTTC	352						
Qy	62	AGCAAGGTGGTTCGTTAACCGGAGAACTGCCATCCACCTCCCGCTACTACAGGCCGC	121						
Db	353	AGCAGGTGGTCCGTTAACCGGAGAACTGCCATCCACCTCCCGCTACTACAGGCCGC	412						
Qy	122	TACTGGACCATGTGGAAAGCTGGCCATGTTGGCTGCAACGCCAACCCAGGTGACA	181						
Db	413	TACTGGACCATGTGGAAAGG-TGCTTAATGTCGCTGCAACTAGGTGCTCA	471						
Qy	182	GGACCTGGGAGGCCATCAAATCCTAACCGGCTTCCACCGGCTCATGGCTICGA	241						
Db	472	TGAGGTGGGGAGCTCAAGAAGGTACCTCTAGCCCTATGTCGGCTTCATGGCTICGA	531						
Qy	242	CAACATCAGGAGGAGGAGTGGTCAAGCTCATGGCTTAAGGCCGGAGCGA	298						
Db	532	CAACCTGCCAAGTGGCTAGCTGCTCAAGCTTATGCCAACGGGTGGCA	588						
RESULT 13									
LOCUS	AB020944	Agropyron intermedium DNA for ribulose-1,5-bisphosphate carboxylase/oxygenase	604 bp	DNA	linear	PLN 27-JAN-2001			
DEFINITION		small subunit, partial cds, clone Agr-A.							
ACCESSION	AB020944						AB020954	787 bp	DNA
VERSION	AB020944.1	GI:4038692					DEFINITION	ribulose-1,5-bisphosphate carboxylase/oxygenase	linear
KEYWORDS		Small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase.					AB020954	small subunit, partial cds,	ribulose-1,5-bisphosphate carboxylase/oxygenase
ORGANISM		Thinopyrum intermedium					AB020954.1	clone Ura-B.	
		Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Thinopyrum.					GI:4038712		
REFERENCE		1 (sites)					KEYWORDS	Small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase.	
AUTHORS		Sasanuma, T. and Miyashita,N.T.					ORGANISM	Triticum urartu	
TITLE		Subfamily divergence in the multigene family of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcs) in Triticeae and its relatives					JOURNAL	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Thinopyrum.	
JOURNAL		Genes Genet. Syst. 73 (5), 297-309 (1998)					JOURNAL	Genes Genet. Syst. 73 (5), 297-309 (1998)	
MEDLINE	99185472						JOURNAL	MEDLINE 99185472	
PUBMED	10085553						PUBLMED	10085553	
FEATURES	2 (bases 1 to 604)						REFERENCE	2 (bases 1 to 787)	
AUTHORS	Sasanuma,T.						AUTHORS	Sasanuma,T.	
TITLE	Direct Submission						TITLE	Direct Submission	
JOURNAL	Submitted [09-DEC-1998] Tsuneo Sasanuma, Kyoto University, Laboratory of Plant Genetics, Graduate School of Agriculture, Sakyo-ku, Kitashirakawa, Oiwakecho, Kyoto, Kyoto 606-8500, Japan (E-mail:sasanuma@kais.kyoto-u.ac.jp), Tel: 81-75-753-6145 (ex. 6145), Fax: 81-75-753-6146)						JOURNAL	Submitted [09-DEC-1998] Tsuneo Sasanuma, Kyoto University, Sakyo-ku, Kitashirakawa Oiwakecho, Kyoto, Kyoto 606-8502, Japan (E-mail:sasanuma@kais.kyoto-u.ac.jp), Tel: 81-75-753-6145 (ex. 6145), Fax: 81-75-753-6146)	
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								/db_xref="taxon:4572"	

/clone="Ura-B"		
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BASE COUNT	185 a 222 c 197 g 183 t	
ORIGIN		
Query Match	59.5%; Score 192.2; DB 8; Length 787;	
Best Local Similarity	80.1%; Pred. No. 3.2e-26;	
Matches	238; Conservative 0; Mismatches 58; Indels 1; Gaps 1;	
Qy	2 GACCTGCTGAAGCAGGTGGACTACTGTCGCAACGGCTGGATAACCCCTCCCTCGAGTC 61	Query Match 59.5%; Score 192.2; DB 8; Length 895;
Db	489 GCCTCTCTGAGCAGGTGGACTACTCTGATGCCAAAGTGGTCCAAGTGGTCCCTCGAGTC 548	Best Local Similarity 79.0%; Pred. No. 3.2e-26;
Qy	62 AGCAAGGTGGCTTGCTGTPAACCGGAGAACTCCACCTCCCGTCTACTAAGCAGGGCCGC 121	Mismatches 63; Indels 1; Gaps 1;
Db	549 AGCAAGGTGGCTTGCTGTPAACCGGAGAACTACAGCTCCCGGTTACTAAGCAGGGCCG 608	/codon_start=1
Qy	122 TACTGACCATGGAAAGATGCCATGGCCTGAGCAGCAGGTGTTACA 181	/product="small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase"
Db	609 TACTGACCATGGAAAGT-GTCCCTATGTTGGTGCACGCCAACAGGTGCTCA 667	/carboxylate (RuBPC)"
Qy	182 GGAGCTGCTGAAGGCCCATCAAACTTACCTACCGGGACCCCTTCACCGCGTCAATCGCTTCGA 241	/EC number="4.1.1.39"
Db	668 CGAGGTGAGGAGGTCAAGAAGGTACCCCTGAGCCTATGTCGGCTCA 727	/protein_id="BAE0539_1"
Qy	242 CAACATCAAGCAGCAGCTGCTCAGCTTACGGCTTAAGGCCCGGGCAGCGA 298	/db_xref="GI:218210"
Db	728 CAACCTGGCCAGTGCAGTGCCTCAAGGCCACCGGGTTSCGA 784	/translation="MAPTQMAASSATSVAPPFOGLKSTAGLPVSRSSGSLGSVSNGCRIRCMQ YRPIEGKRKETLSYLPLUSTLRLKQDYLRSKFLERSKVGPFREHSSPGI YDGRYWTMWKLPMNGCTDATQVNVEEVKEYPDATVRVIGTPEAKAYPDAFIRIGDFNTRQVOLIS PFLAYKPPGCBESGGN"
RESULT 15		
RICRUBPC2	895 bp mRNA linear	PLN 23-MAR-2002
LOCUS	Oryza sativa (japonica cultivar-group) mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone	PLN 23-MAR-2002
DEFINITION		05SS106.
VERSION	D00644.1 GI:218209	Search completed: November 27, 2003, 19:00:06
KEYWORDS	RUBPC; ribulose-1,5-bisphosphate carboxylase	Job time : 1984 secs
SOURCE	Oryza sativa (japonica cultivar-group)	
ORGANISM	Oryza sativa (japonica cultivar-group)	
Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta; Ehrhartioideae; Oryzae; Oryza.		
REFERENCE	Matsuoka, M., Kano-Murakami, Y., Tanaka, Y., Ozeki, Y. and Yamamoto, N.	
AUTHORS	Classification and nucleotide sequence of cDNA encoding the small	
TITLE	subunit of ribulose-1,5-bisphosphate carboxylase from rice	
SOURCE	Plant Cell Physiol. 29, 1015-1022 (1988)	
ORGANISM	These data kindly submitted in computer readable form by: Makoto	
JOURNAL	Matsuoka	
COMMENT	National Institute of Agrobiological Resources	
	Tsukuba Science City	
	Ibaraki 305	
	Japan	
	Phone: 0298-38-8381	
	Fax: 0298-38-8199.	
FEATURES	Location/Qualifiers	
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 QY 242 CAACATCAAGCAACGCAAGTGCTAGCTCATGCCATAAACGC 286
 Db 799 CAACTTAGGCCAGCTGCACTAGCTCATCGCTCATCGCTCAACCC 843

RESULT 3
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 ID ABL93405 standard; cDNA; 471 BP.
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 AC ABL93405;
 XX 10-JUN-2002 (first entry)
 XX Arabidopsis thaliana nucleic acid sequence Ref:2027170 SEQ ID NO:170.
 DE Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
 KW genetic modification; gene; ss.
 KW Arabidopsis thaliana.
 XX US2002023280-A1.
 XX 21-FEB-2002.
 XX 26-JAN-2001; 2001US-0770444.
 XX 27-JAN-2000; 2000US-178502P.
 XX (GORLACH J.
 PA (ANYY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYU/) YU Y.
 PA (RAMEKA J G.
 PA (PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.

XX Gorlach J, An Y, Hamilton CM, Price JB, Raines TM, Yu Y,
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,
 PI Hurban P;
 DR 2002-267486/31.

XX New *Arabidopsis thaliana* nucleic acid, for identifying homologous
 PT genes, producing compositions that modulate the expression or function
 PT of its encoded protein, and mapping functional regions of a protein -
 XX
 PS SEQ ID 170; 44pp; English.

CC functional regions of the proteins, and in studying associated
 CC physiological pathways. (1) can also be used: (1) For the genetic
 CC manipulation of cells, particularly plant cells; (2) in screening assays
 CC of various plant strains to determine the strains that are best capable
 CC of withstanding a particular disease or environmental stress; (3) For
 CC enhancing or inhibiting production of a biosynthetic product in a plant;
 CC (4) as probes in mapping and in diagnosis, in genetic modification and
 CC for screening purposes, to generate additional copies of the nucleic
 CC acids, to generate ribozymes or antisense oligonucleotides, and as
 CC single stranded DNA probes or as triple-strand forming oligonucleotides;
 CC and (5) for generating genetically modified transgenic organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.

XX Sequence 471 BP; 140 A; 94 C; 97 G; 140 T; 0 other;

SQ Query Match 38.9%; Score 125.6; DB 24; Length 471;
 Best Local Similarity 67.8%; Pred. No. 2.5e-18;
 Matches 206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;

QY 1 CGACCTCGTGAACCGACTACCTGCTGCCAACCGCTGATAACCTGCTGCCTGAGCT 60
 Db 464 CGATATTGCTTCTCCCAACAGTGTATCTTGTGTTGATTCTTGTGTTGATT 405

QY 61 C--AGZAGGTGGCTTCGTTACCGGAGACTCCACCTCCGGCTACTACAGGAG 117
 Db 404 CGAGTTAGGACGGATTGTGTAACCTGAGCACGGAAAACACTCCGGATACTACAGATGG 345

QY 118 CCCCTACTGGACCATGGAAAGCATGGCCATGTTGGGTGAAACGACGCCACCCAGGT 177
 Db 344 ACGGTACTGGCATATGGTGAACGC-TTCCATTGTTGATGACCGACTCCGGTCAAGTGT 286

QY 178 ACAGAGACGCTGCCAGGGCCATCAATCTACCGGAGCCATCAATCTACGGCTCATCGCT 237
 Db 285 TGAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 226

QY 238 TCGACAACATCAAGCAAGCCAGCTGCTCATCGCTTCAAGCCGGCAGCG 297
 Db 225 TCCACAAACACCCGGTCAAGTCCAAATGCACTAGCTTCAATGGCTTCAAGGCCCGAGCTICA 166

QY 298 ACTA 301
 Db 165 CCGA 162

RESULT 4
 AAC4B433 AAC4B433 standard; DNA; 546 BP.
 ID AAC4B433
 XX AAC4B433;
 AC AAC4B433;
 XX DT 18-OCT-2000 (first entry)

XX PD 06-SEP-2000.
 XX PP 25-FEB-2000; 20000EP-0301439.
 DE Arabidopsis thaliana DNA Fragment SEQ ID NO: 57460.
 XX PR 25-FEB-1999; 99US-0121825.
 KW Hybridisation assay; Genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX OS Arabidopsis thaliana.
 PN BP1033405-A2.

XX The present invention describes an *Arabidopsis thaliana* nucleic acid (I)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence (S1) selected from any one of the 999 sequences given in
 ABL9336 to ABL94234. (I) have insecticide and fungicide activities, and
 CC they can be used as protein expression modulators. (I) can be used in
 CC identifying homologous or related genes, in producing compositions that
 CC modulate the expression or function of their encoded proteins, mapping

PR	29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR	01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR	02-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR	08-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR	16-APR-1999;	99US-0139845.	PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
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PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-014519.
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PR	20-MAY-1999;	99US-0134941.	PR	02-AUG-1999;	99US-0146586.
PR	21-MAY-1999;	99US-0134219.	PR	02-AUG-1999;	99US-0146388.
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PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
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PR	18-JUN-1999;	99US-0139462.	PR	26-AUG-1999;	99US-0150884.
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PR	18-JUN-1999;	99US-0139461.	PR	15-SEP-1999;	99US-0154018.
PR	22-JUN-1999;	99US-0139461.	PR	16-SEP-1999;	99US-0154039.
PR	30-JUN-1999;	99US-014117.	PR	31-AUG-1999;	99US-0151303.
PR	01-JUL-1999;	99US-013999.	PR	01-SEP-1999;	99US-0151303.
PR	01-JUL-1999;	99US-0140353.	PR	01-SEP-1999;	99US-0151303.
PR	02-JUL-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0140823.	PR	23-SEP-1999;	99US-0155659.
PR	29-JUN-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0156459.
PR	09-JUL-1999;	99US-0140991.	PR	28-SEP-1999;	99US-0156596.
PR	12-JUL-1999;	99US-0142920.	PR	29-SEP-1999;	99US-0157117.
PR	13-JUL-1999;	99US-0142977.	PR	04-OCT-1999;	99US-0157733.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144005.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.

06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142303.
PR 09-JUL-1999; 99US-0142220.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144055.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-01444884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145911.
PR 27-JUL-1999; 99US-0145912.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148565.
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PR 16-AUG-1999; 99US-0149568.
PR 17-AUG-1999; 99US-014975.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 27-AUG-1999; 99US-0149929.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-014930.
PR 07-SEP-1999; 99US-0152363.
PR 13-SEP-1999; 99US-0153058.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154179.
PR 22-SEP-1999; 99US-0155139.

PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-015984.
PR 21-OCT-1999; 99US-016041.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160816.
PR 22-OCT-1999; 99US-016080.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-016104.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161320.
PR 28-OCT-1999; 99US-0161392.
PR 28-OCT-1999; 99US-0161393.
PR 29-OCT-1999; 99US-0162442.

Query Match 38.9%; Score 125.6%;
Best Local Similarity 68.6%; DB 21; Length 572;
Matches 203; Conservative 0; Mismatches 89; Indels 8 4; Gaps 2;
Qy 1 CGACCTGCTGAAGCAGGTGGACTACCTGCTGGCAAGGGCTGATCCCTGCCTCGAGTT 60
Db 266 CGAATTCGCTTAAAGAACATTGACTACCTTATCGCAACAAGTGGATTCCTGGTGTGATT 325
Qy 61 C---AGAAAGGTCGGCTGGTACCCGAGAACCTCCACCTCCCCGGCTACTACGACGG 117
Db 326 CGAGTGGAGCAGGATTGTGTGACATGGTAAGTGGTAAGCCTGAGCAGGTAACTCAGATGATGTT 385
Qy 118 CCCTCTACTGGACCATGGGAACCATGGCAACCTGCTGACGAGCCACCCAGTGT 177
Db 386 ACCTGATCTGGACATGGTAAGTGGTAAGCCTGAGCAGCTCCGGTCAAGTGT 444
Qy 178 ACAAGGAGCTGAGGAGCCATCAAATCCTACCGGAGCCTTCCACGGGTACATGGCT 237
Db 445 TGAGGAGTGGAGAGTGAGACTGGCTGAGAAGTACCCATAGCTGCTCATAGGGAT 504
Qy 238 TCCACAAAGATCAAGCAGCCAGTGGCTCAGCTTCACTGCCTTCAAGGCCCGGC 293
Db 505 TCGAAACACCCGTCAAGTCCACTGATCAGTTCAAGGCCAACAGC 560

RESULT 6
AAC47674 AAC47674 standard; DNA; 599 BP.
XX XX DT 18-OCT-2000 (first entry)
AC AC AAC47674;
XX XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54694.

XX	KW	Hybridisation assay; genetic mapping; gene expression control;	
KW	KW	protein identification; signal transduction pathway;	
KW	KW	metabolic pathway; promoter; termination sequence; B.	
XX	OS	Arabidopsis thaliana.	
XX	XX	EP1033405-A2.	
PN	PN	EP1033405-A2.	
XX	XX	06-SEP-2000.	
PD	PD	25-FEB-2000; 2000EP-0301439.	
XX	XX	25-FEB-1999; 99US-0121825.	
PR	PR	05-MAR-1999; 99US-012310.	
PR	PR	09-MAR-1999; 99US-012358.	
PR	PR	23-MAR-1999; 99US-012578.	
PR	PR	25-MAR-1999; 99US-0126264.	
PR	PR	29-MAR-1999; 99US-0126705.	
PR	PR	01-APR-1999; 99US-0127462.	
PR	PR	06-APR-1999; 99US-0128224.	
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PR	PR	30-APR-1999; 99US-0132048.	
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PR	PR	18-MAY-1999; 99US-0134283.	
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PR	PR	20-MAY-1999; 99US-0135124.	
PR	PR	21-MAY-1999; 99US-0135353.	
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PR	PR	01-JUN-1999; 99US-0137222.	
PR	PR	03-JUN-1999; 99US-0137528.	
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PR	PR	10-JUN-1999; 99US-0138540.	
PR	PR	10-JUN-1999; 99US-0138847.	
PR	PR	18-JUN-1999; 99US-0139119.	
PR	PR	14-JUN-1999; 99US-013952.	
PR	PR	16-JUN-1999; 99US-013953.	
PR	PR	18-JUN-1999; 99US-0139492.	
PR	PR	18-JUN-1999; 99US-013954.	
PR	PR	18-JUN-1999; 99US-013955.	
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PR	PR	18-JUN-1999; 99US-013958.	
PR	PR	18-JUN-1999; 99US-013959.	
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PR	PR	18-JUN-1999; 99US-013961.	
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PR	PR	18-JUN-1999; 99US-013963.	
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PR	PR	18-JUN-1999; 99US-0139763.	
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PR	PR	22-JUN-1999; 99US-0139899.	

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PR	31-AUG-1999;	99US-0151418.		
PR	01-SEP-1999;	99US-0151930.		
PR	07-SEP-1999;	99US-0152363.		
PR	10-SEP-1999;	99US-0153070.		
PR	13-SEP-1999;	99US-0153758.		
PR	15-SEP-1999;	99US-0154018.		
PR	16-SEP-1999;	99US-0154039.		
PR	20-SEP-1999;	99US-0154719.		
PR	22-SEP-1999;	99US-0155119.		
PR	21-SEP-1999;	99US-0155486.		
PR	24-SEP-1999;	99US-0155659.		
PR	28-SEP-1999;	99US-0155695.		
PR	29-SEP-1999;	99US-0156596.		
PR	04-OCT-1999;	99US-0157117.		
PR	05-OCT-1999;	99US-0157753.		
PR	06-OCT-1999;	99US-0157865.		
PR	07-OCT-1999;	99US-0158029.		
PR	08-OCT-1999;	99US-0158232.		
PR	12-OCT-1999;	99US-0158369.		
PR	13-OCT-1999;	99US-0159293.		
PR	14-OCT-1999;	99US-0159294.		
PR	13-OCT-1999;	99US-0159295.		
PR	14-OCT-1999;	99US-0159329.		
PR	14-OCT-1999;	99US-0159330.		
PR	14-OCT-1999;	99US-0159331.		
PR	14-OCT-1999;	99US-0159637.		
PR	18-OCT-1999;	99US-0159638.		
PR	21-OCT-1999;	99US-0159584.		
PR	21-OCT-1999;	99US-0160741.		
PR	21-OCT-1999;	99US-0160767.		
PR	21-OCT-1999;	99US-0160768.		
PR	21-OCT-1999;	99US-0160770.		
PR	21-OCT-1999;	99US-0160814.		
PR	25-OCT-1999;	99US-0161406.		
PR	26-OCT-1999;	99US-0161359.		
PR	26-OCT-1999;	99US-0161360.		
PR	26-OCT-1999;	99US-0161361.		
PR	28-OCT-1999;	99US-0161920.		
PR	28-OCT-1999;	99US-0161993.		
PR	29-OCT-1999;	99US-0162142.		
Qy		Query Match Similarity 38.9%; Best Local Similarity 67.8%; Matches 206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;		
Db	1 CGACCTGCTGAGGCAAGTGGACTACCTGGCTGCAGACGGTGATACTCCCTGGCTCGAGTC 60	Score 125.6; DB 21; Length 599; Pred. No. 2.5e-18;		
Db	290 CGAATTTGCTAGGAATGGTGTGAAACCTGGATACCTGGCTCGAGTC 349	WPI: 2002-47924/51.		
Qy	61 C--AGCAAGTCCGGTTCTCTGAACTGGCATGCCATGTTGGCTGAAAGCTCCACCTCCGGTGTACTAGATCGCG 117	Claim 1, SEQ ID NO 344; 40PP + Sequence Listing; English.		
Db	350 CGAGCTACTGGAACTGGTGTGAAACCTGGATACCTGGCTCGAGTC 409	PI Rameika JG, Page A, MacIver AV, Ledford BL, Woesner JP, Price JL, Raines TM, Yu Y, Hamilton CM, Hoffmann JP, Haas WD;		
Qy	118 CGGCTACTGGACCATTGAGCAAGCAGCTGGCTGAACTGGCTGGTCTGGCTCGAGTC 177	PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffmann N;		
Db	410 AGGGTACTGGAACTGGTGTGAAACCTGGATACCTGGCTCGAGTC 468	PI Hurlan P;		
Qy	178 ACAGGGCTGGAGGGCCATCAATCTAACCTGAGGAACTGGCTGGCTGGCTCGAGTC 237	XX DR WPI: 2002-47924/51.		
Db	469 TGAAGGGATGTTGAGAATGCAAGAAGGATCCGGCGCTTCATAGATCATCGGT 528	CC PT New nucleic acid that hybridizes to <i>Arabidopsis thaliana</i> sequences, useful e.g. for preparing transgenic plants with increased resistance or altered metabolism -		
Qy	238 TCGACAACTAACGAGCAGCTGGCTTAGTTCTACAGGCCCGGCG 297	CC CC PT The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66122) or their fragments (II) are used to express the corresponding polypeptides (III) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics).		
Db	529 TCGACAACTAACCGCTCAAGTCATGATCAGTTCTACAGGCCCGGCGCTTCATCGGT 588	CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at seqdata.uspto.gov/sequence.html?docID=99990970149.		
Qy	298 ACTA 301	CC CC		

XX	SQ Sequence 681 BP; 183 A; 143 C; 160 G; 195 T; 0 other;	XX	SQ Sequence 724 BP; 198 A; 174 C; 156 G; 196 T; 0 other;
Query Match 38.9%; Best Local Similarity 68.6%; Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;	Score 125.6; DB 24; Length 681; Pred. No. 2.5e-18; Best Local Similarity 68.6%; Matches 203; Conservative 0; Mismatches 90; Indels 4; Gaps 2;	Query Match 38.9%; Best Local Similarity 67.8%; Pred. No. 2.5e-18;保守性 206; 错配 90; 插入 4; 缺口 2;	Score 125.6; DB 24; Length 724;保守性 206; 错配 90; 插入 4; 缺口 2;
Qy 1 CGACCTGCTGAAGCAGGTGGACTACTGCTGGCAACGGCTGGATACCCCTGCCCTGCACTT 60	Qy 1 CGACCTGCTGAAGCAGGTGGACTACTGCTGGATACCCCTGCCCTGCACTT 60	Qy 1 CGACCTGCTGAAGCAGGTGGACTACTGCTGGATACCCCTGCCCTGCACTT 60	Qy 1 CGACCTGCTGAAGCAGGTGGACTACTGCTGGATACCCCTGCCCTGCACTT 60
Db 472 CGAATTGGCTTAAGGAGTTGACTACCTTCCTCGCAACAAATGGATTCTGTGTGAATT 413	Db 279 CGAATTGGCTTAAGGAGTTGACTACCTTCCTCGCAACAAATGGATTCTGTGTGAATT 338	Db 279 CGAATTGGCTTAAGGAGTTGACTACCTTCCTCGCAACAAATGGATTCTGTGTGAATT 338	Db 279 CGAATTGGCTTAAGGAGTTGACTACCTTCCTCGCAACAAATGGATTCTGTGTGAATT 338
Qy 61 C---AGCAAGGTGGCTTCTGTGACCGGAGAACTCCACCTCCGGTGTACTAACAGCGG 117	Qy 61 C---AGCAAGGTGGCTTCTGTGACCGGAGAACTCCACCTCCGGTGTACTAACAGCGG 117	Qy 61 C---AGCAAGGTGGCTTCTGTGACCGGAGAACTCCACCTCCGGTGTACTAACAGCGG 117	Qy 61 C---AGCAAGGTGGCTTCTGTGACCGGAGAACTCCACCTCCGGTGTACTAACAGCGG 117
Db 412 CGAGTTGGACGACGGATTGTGACCGTAGCACGGAAACTCCGGATACTACAGATG 353	Db 339 CGACTTAGGACGACGGATTGTGACCGTAGCACGGAAACTCCGGATACTACAGATG 398	Db 339 CGACTTAGGACGACGGATTGTGACCGTAGCACGGAAACTCCGGATACTACAGATG 398	Db 339 CGACTTAGGACGACGGATTGTGACCGTAGCACGGAAACTCCGGATACTACAGATG 398
Qy 118 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 118 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 118 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 118 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237
Db 352 ACGGTACTGCGATTGAAAGC- TTCCATTGTTGAAAGC- 294	Db 399 ACGGTACTGCGATTGAAAGC- TTCCATTGTTGAAAGC- 457	Db 399 ACGGTACTGCGATTGAAAGC- TTCCATTGTTGAAAGC- 457	Db 399 ACGGTACTGCGATTGAAAGC- TTCCATTGTTGAAAGC- 457
Qy 178 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 178 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 178 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237	Qy 178 ACAAGGAGCTGCAAGGGCATCAATCATACCGGACCCCTTCCACCGCTCATCGCT 237
Db 293 TGAAAGCAACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATAGGATCATCGCTA 234	Db 458 TGAAAGCAACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATAGGATCATCGCTA 517	Db 458 TGAAAGCAACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATAGGATCATCGCTA 517	Db 458 TGAAAGCAACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATAGGATCATCGCTA 517
Qy 238 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 293	Qy 238 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 297	Qy 238 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 297	Qy 238 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 297
Db 233 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 178	Db 518 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 178	Db 518 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 178	Db 518 TCGACAACACTCAAGGAGCAATGGAAAGGAGACTACCGGGCCCTCATCGCTA 178
RESULT 8	RESULT 8	RESULT 9	RESULT 9
AB149453 AB149453 standard; cDNA; 724 BP.	ABK30640 ABK30640 standard; cDNA; 724 BP.	ABK30640 ABK30640	ABK30640 ABK30640
XX ID	XX ID	XX XX	XX XX
AC ABI49453;	AC ABI49453;	AC ABK30640;	AC ABK30640;
XX DT 01-JUL-2002 (first entry)	XX DT 23-APR-2002 (first entry)	XX DE 23-APR-2002	XX DE 23-APR-2002
DB Sequence #55 used to create transgenic plant with dwarf phenotype.	DB Plant dwarfing/stunting related cDNA seq ID 54.	DB KW	DB KW
KW Transgenic plant; dwarf phenotype; ss.	KW Plant; ss; dwarfism; stunting; EST; expressed sequence tag;	KW	KW
XX KW	XX KW	XX KW	XX KW
XX OS Arabidopsis thaliana.	XX OS Arabidopsis thaliana.	XX OS	XX OS
XX PN WO200208411-A2.	XX PN WO200208411-A2.	XX PD 31-JAN-2002.	XX PD 31-JAN-2002.
XX PD 31-JAN-2002.	XX PD 31-JAN-2002.	XX XX	XX XX
XX PF 20-JUL-2001; 2001WO-US233315.	XX PF 20-JUL-2001; 2001WO-US233315.	XX PR 20-JUL-2000; 2000US-219809P.	XX PR 20-JUL-2000; 2000US-219810P.
XX PR 20-JUL-2000; 2000US-219943P.	XX PR 20-JUL-2000; 2000US-219943P.	XX PA 20-JUL-2001; 2001WO-US231120.	XX PA 20-JUL-2001; 2001WO-US231120.
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.	XX PA (LARG-) LARGE SCALE BIOLOGY CORP.	XX PA (DOW CHEM CO.) DOW CHEM CO.	XX PA (DOW CHEM CO.) DOW CHEM CO.
XX Pogue GP, Della-Cioppa GR, Wolfe GM, Zheng W;	XX Pogue GP, Della-Cioppa GR, Wolfe GM, Zheng W;	XX PA (REDD/) REDDY S. A.	XX PA (REDD/) REDDY S. A.
XX DR 2002-195875/25.	XX DR 2002-195875/25.	XX PA (LARR/) LARRINDA M. I.	XX PA (LARR/) LARRINDA M. I.
XX PT Creating transgenic plants exhibiting a dwarf phenotype useful in biopharmaceutical manufacturing, comprises expressing in the plant a gene for dwarfism or stunting having a sequence selected from 122 polynucleotide sequences.	XX PT Creating transgenic plants exhibiting a dwarf phenotype useful in biopharmaceutical manufacturing, comprises expressing in the plant a gene for dwarfism or stunting having a sequence selected from 122 polynucleotide sequences. This sequence represents one of those polynucleotide sequences. The nucleic acid and amino acid sequences are useful for producing transgenic plants exhibiting a dwarf phenotype for use in biopharmaceutical manufacturing. The cDNA sequences may be used in recombinant DNA molecules to direct expression of polypeptides in appropriate host cells.	XX PA (RUEG/) RUEGER M.	XX PA (RUEG/) RUEGER M.
XX PS Claim 1; Page 154, 178pp; English.	XX PS Claim 1; Page 154, 178pp; English.	XX PA (WEGL/) WEIGLARZ T.	XX PA (WEGL/) WEIGLARZ T.
XX CC This invention relates to the creation of a transfected or transgenic plant selected from ornamental, horticultural, forestry, medicinal and Nicotiana sp. plants, all of which exhibit a dwarf phenotype by expressing in the plant a DNA comprising a sequence selected from 122 polynucleotide sequences. This sequence represents one of those polynucleotide sequences. The nucleic acid and amino acid sequences are useful for producing transgenic plants exhibiting a dwarf phenotype for use in biopharmaceutical manufacturing. The cDNA sequences may be used in recombinant DNA molecules to direct expression of polypeptides in appropriate host cells.	XX CC This invention relates to the creation of a transfected or transgenic plant selected from ornamental, horticultural, forestry, medicinal and Nicotiana sp. plants, all of which exhibit a dwarf phenotype by expressing in the plant a DNA comprising a sequence selected from 122 polynucleotide sequences. This sequence represents one of those polynucleotide sequences. The nucleic acid and amino acid sequences are useful for producing transgenic plants exhibiting a dwarf phenotype for use in biopharmaceutical manufacturing. The cDNA sequences may be used in recombinant DNA molecules to direct expression of polypeptides in appropriate host cells.	XX PA (BLAK/) BLAKESLEE B.	XX PA (BLAK/) BLAKESLEE B.
XX CC PI Reddy SA, Larinuua MI, Ruegger M, Weglarz T, Blakeslee B, Oriendo VBJ, Savickas JP, McCrary AD, Miller AB, Della-Cioppa RG, Wolfe MG, Zheng W, Gachotte D, Grosley R,	XX CC PI Reddy SA, Larinuua MI, Ruegger M, Weglarz T, Blakeslee B, Oriendo VBJ, Savickas JP, McCrary AD, Miller AB, Della-Cioppa RG, Wolfe MG, Zheng W, Gachotte D, Grosley R,	XX PA (ORIE/) Oriendo V B J.	XX PA (ORIE/) Oriendo V B J.
CC (MCRR/) MCERRY A D.	CC (MCRR/) MCERRY A D.	PA (MILL/) MILLER A B.	PA (MILL/) MILLER A B.
CC (GACH/) GACHOTTE D.	CC (GACH/) GACHOTTE D.	PA (WEGL/) WEIGLARZ T.	PA (WEGL/) WEIGLARZ T.
CC (GROS/) GROSLEY R.	CC (GROS/) GROSLEY R.	PA (PELL/) PELL R.	PA (PELL/) PELL R.

WPI; 2002-164823/21.

Polynucleotide and amino acid sequences identified in one or more metabolic pathways that lead to dwarfism and stunting in plants, useful in agriculture to create dwarf varieties of any plant species -

Example 10; Fig 1, 717pp; English.

The invention relates to polynucleotide and amino acid sequences identified in one or more metabolic pathways that lead to dwarfism and stunting in plants. Also included are vectors comprising the polynucleotides transgenic plants (including the seed and leaf) transfected with the polynucleotides or vectors, a process for altering the metabolism of a plant comprising providing the above vector and a plant, and transfecting the plant with the vector under conditions such that the metabolism of the plant is altered by expression of the isolated nucleic acid from the vector, e.g. such that a stunting phenotype in an industrial plant is produced and a process for the characterisation of fractionated biological samples, comprising (a) providing one or more fractionated biological samples, references samples, a gas chromatograph apparatus, a mass spectroscopy apparatus or data analysis software and (b) treating the fractionated biological samples and the reference samples with the gas chromatography apparatus to generate chromatographic data corresponding to the fractionated biological samples and the reference samples, (c) treating the fractionated biological samples and the reference samples with the mass spectrometry apparatus to generate spectroscopic data corresponding to the fractionated biological samples and the reference samples and (d) processing the chromatographic and the spectroscopic data with the data analysis software. The nucleic acid and the vector are useful for altering the metabolism of a plant and for stunting a plant. The nucleic acids are useful in agriculture to create dwarf varieties of any plant species. The present sequence is a plant EST, expressed sequence tag, isolated from a cDNA library and related to stunting/dwarfism.

Sequence 724 BP; 198 A; 174 C; 156 G; 196 T; 0 other;
Cherry March 38 @. Score 125.6: DB 24: Length 724;

Qual. vac. Ch. Best Local Similarity 67.8%; Pred. NO. 2.5e-18; Mismatches 0; Indels 4; Gaps Matches 206; Conservative

1	CGACCTGCTGAAAGGTGGACTCTGCTGGCAAGGCTCGATACCCTGCTCGAGTT	6
279	CGACCTGCTGAAAGGTGGACTCTGCTGGCAAGGCTCGATACCCTGCTCGAGTT	3

61 C---AGCAAGGTGGCTTCTGTAAACCGGAGAACTCCACCTCCCGTGCTACTACGAGCG
2 3 CTTTAAACCTTTC

399 ACGGTACTGGACAAATGTGAAAGC- TTCCATTGTTCGGATCGAACCGAATCCGTCCTAAGTGT 4

518 TCGACAAACACCCGTCAAGTCAAATGCAATTGTTCAATTGCCCTAACAGCCCCAAGCTTCA 5
509 ^AC_nT_m 101

Y 420 AJA 394
o 578 CCGA 581

0
ESSM11
02/2010

D UBK30788 standard; CDNA; 726 BP.
X ^PDK30789.

XX	Sequence	726 BP; 194 A; 180 C; 156 G; 196 T; 0 other;	PA	(HOFFMAN N. (HURBAN P.)
Query Match	38.9%; Score 125.6; DB 24; Length 726;	XX	PI	Gorlach J., An Y., Hamilton CM, Price JT, Raines TM, Yu Y;
Best Local Similarity	67.8%; Pred. No. 2.5e-18;	XX	PI	Ledford BL, Woessner JP, Haas WD;
Matches 206; Conservative 0; Mismatches -94; Indels 4; Gaps 2;	XX	PI	Rameka JG, Page A., Mathew AV,	
Qy	1 CGACCTGTGAAGAGGTGCAACTGTGCAACGGTGGATAACCTGGCTGAGTT 60	XX	PI	Kricker M., Slater T., Davis KR, Allen K., Hoffman N., Hurban P;
Db	281 CGAATTGGCTAAAGGATGACTACCTTCCTCCGTAACAAGTGATTCTGTGTAATT 340	XX	DR	WPI; 2002-400781/43.
Qy	61 C---AGCAAGGTGGTCAAGGACTCTGGTACCGTACCTGGCTACTACGACCG 117	PT	New <i>Arabidopsis thaliana</i> nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein -	
Db	341 CGAGTAGACCGGAACTCGGATACGTAGATCGGAACTCGGATACGTAGATGG 400	PS	Claim 1: SEQ ID NO 918: 49pp + Sequence Listing; English.	
Qy	118 CGCCTACTGGACCATGTGGAAGCATGCCATGTGGCTGCAAGACGCCAACCGAGGT 177	XX	The invention relates to an <i>Arabidopsis thaliana</i> nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 939 sequences (ABN98233-ABN99231), given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying associated physiological pathways. (I) is also useful for the genetic manipulation of cells, particularly plant cells. (I) is also useful in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress. (II) and (III) are useful in improved methods of treating crops to enhance their tolerance to environmental stress. (I) is also useful for elucidating biochemical pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening programs to identify agents that mimic or enhance the action of tolerance factors. Such agents are useful in improved methods of treating crops to enhance their tolerance to environmental stress. (I) is also useful for enhancing or inhibiting production of a biosynthetic product in a particular plant, for identifying other mediators that may induce expression of proteins of interest, for establishing the extent to which any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress, for identifying factors involved in biosynthetic pathways of nutritional, commercial, or medicinal value and for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=9990977045.	
Db	401 ACTGTTACTGGACATGTGGAAAGC-TTCCATGGTGGATCGCTCAAAGT 459	CC	Qy	38.9%; Score 125.6; DB 24; Length 771;
Qy	178 ACAGAGCTGCACAGGGCCATCAAATCCACCCCTTCCACCGCGTCATCGGCT 237	CC	Best Local Similarity 67.8%; Pred. No. 2.5e-18;	
Db	460 TGAGGAATGTGAGAATGAAAGGAGTACCGGCTTCAATTAGATCATGGAT 519	CC	Matches 206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;	
Qy	238 TCCACAAATCAGCAGACGCACTGGCAGCTCAGCTTCAAGGCCGGCAGCG 297	CC	Qy	1 CGACCTGTGAAGCAGGTGGACTACCTGCTGGCAACGGCTGATACCTGGCTGAGTT 60
Db	520 TCCACAAACCCCTCAAGTCAAATGCAATGCAATGTTCAATCCCTAACAGCTTCA 579	CC	Db	449 CGAATTGGCTAGGAGTTGACTACCTTCCTGGCAAGTGGATCTTGTGTTGAATT 390
Qy	298 ACTA 301	CC	Qy	61 C---ACCAAGGTGACCATGGGAACTCCGAGACTCACCTCCGGTCACTACGACGG 117
Db	580 CCSA 583	CC	Db	389 CGAGTTAGGACGGATTGACCTGAGAACCTCCGGATACTACGATGCG 330
RESULT 11		XX	Qy	118 CGGCTACTGGACCATGGGAACTCCGAGACTCACCTCCGGTCACTACGACGG 177
ID ABN9150/C	ABN9150 standard; DNA; 771 BP.	XX	Db	329 ACGGTACTGGCAATGGGAACTCCGAGACCTGGCTCAATGGTCAATGTT 271
AC	AC	XX	Qy	178 ACAAGGAGCTGGGGCACTGAAATCCTAACGGAGCTCATCGCT 237
DT	01-AUG-2002 (first entry)	XX	Db	270 TGAAGGAGCTGGTAAAGGATGCAAGAAGCTGGCCCTTCATAGGATCATCGGT 211
DE	Arabidopsis thaliana expressed polynucleotide SEQ ID NO 918.	XX		
KW	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress; disease; crop; thale cress; tolerance factor; insect; pathogen; nutrition; ds.	XX		
KW	Arabidopsis thaliana.	OS		
KW	US2002023281-A1.	PN		
KW	21-FEB-2002.	PD		
XX	26-JAN-2001; 2001US-0770445.	PF		
XX	27-JAN-2000; 2000US-178472P.	PR		
XX	(GORLACH J.	PA		
PA	(ANYY.) AN Y.	PA		
PA	(HAMIL.) HAMILTON C M.	PA		
PA	(PRIC.) PRICE J L.	PA		
PA	(RAIN.) RAINES T M.	PA		
PA	(YUYU.) YU Y.	PA		
PA	(RAME.) RAMEKA J G.	PA		
PA	(PAGE.) PAGE A.	PA		
PA	(MATH.) MATHEW A V.	PA		
PA	(LEDF.) LEDFORD B L.	PA		
PA	(WOES.) WOESSNER J P.	PA		
PA	(HAAS.) HAAS W D.	PA		
PA	(GARC.) GARCIA C A.	PA		
PA	(KRIC.) KRICKER M.	PA		
PA	(SLAT.) SLATER T.	PA		
PA	(DAVI.) DAVIS K R.	PA		
PA	(ALLE.) ALLEN K.	PA		

Qy 238 TCGACAACATCAAGCAGCCAGCTAGCTCATGCCCTAACAGCCCCGGGAGCG 297
 Db 21.0 TCGACAACATCAAGCAGCTAACGTCATAGCTTCAAGCCAAAGCTCA 151

Qy 298 ACTA 301
 Db 150 CCGA 147

RESULT 12
 ABN99094/c standard; DNA; 785 BP.
 AC ABN99094/
 XX ID ABN99094
 DT 01-AUG-2002 (first entry)
 XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 862.
 KW Arabidopsis thaliana; Plant; insecticide; fungicide; transgenic; stress; disease; crop; thale cress; tolerance factor; insect; pathogen; nutrition; ds.
 XX Arabidopsis thaliana.
 OS US200203281-A1.
 PN XX
 PD 21-FEB-2002.
 PF 26-JAN-2001; 2001US-07070445.
 PR XX
 27-JAN-2000; 2000US-178472P
 XX (GORL/) GORLACH J.
 PA (ANYY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (TOY/) YU Y.
 PA (RAMEAKA J G.
 PA (PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LBDF/) LEDFORD B L.
 PA (WOESNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARCI/) GARCIA C A.
 PA (KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.

XX New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein -

PT PT
 XX XX
 PS Claim 1: SEQ ID NO 862; 49pp + Sequence Listing; English.

XX The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is

CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stresses. (I) is also useful
 CC for enhancing or inhibiting production of a biosynthetic product in a
 CC plant. (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and
 CC for identifying products of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the Printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/Sequence.html?DocID=9990977045.

XX Sequence 785 BP; 226 A; 155 C; 193 G; 211 T; 0 other;

SQ Query Match 38.9%; Score 125.6; Pred No. 2.5e-18;
 Best Local Similarity 68.6%; Pred No. 2.5e-18;
 Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;

Db Qy 1 CGACCTGTGAAGCAGTTGGACTACCTGCTGGCAAGGCTGATCCCTGCAGTT 60
 Db 531 CGATATGGCTTAAGGAAGTTGACTACCTTATCGCAAGAGTGATTCCTGGTTGATT 472

Db Qy 61 C---AGCAAGGTGGCTGTGTTACCGGAGACTCCACCTCCCGGCTACTACGAGGG 117
 Db 471 CGAGTGTGGACGACGGATTGTGTAACCTGTGAGCAAGCTGATCTATGATGG 412

Db Qy 118 CCCCTACTGGACCATTGTTGAAGGATGCCATGTTGGCTGDAACAGCCACCCAGGTGT 177
 Db 411 ACGGTACTGGCATATGGAAAGC-TTCCCCTGGTTGACCGACTCCGCTCAAGTGT 353

Db Qy 178 ACAAGGAACTCTGGAGGCCCCATCAAATCCTAACCGGAGCTCATCGCT 237
 Db 352 TGAGGAGTGGAGTGGAGTGAAGGATGCCAAATGCTCTATAGGATCATCGAT 293

Db Qy 238 TCGACAAACATCAAGGAGACGCAAGTGGCTCAGCTTCAATGCCCTAACAGCCCCGGC 293
 Db 292 TCGACAAACACCCCTCAACTCCACTGATCGATTCATGGCTAACAGCACCAGC 237

RESULT 13
 AAC52133 ID AAC52133 standard; DNA; 1164 BP.
 XX AC AAC52133;
 XX DT 18-OCT-2000 (first entry)
 DB DE XX
 Arabidopsis thaliana DNA fragment SEQ ID NO: 70444.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.

PN	EP1033405-A2.		99US-0142154.
XX		PR	01-JUL-1999;
PD	06-SEP-2000.	PR	02-JUL-1999;
XX	25-FEB-2000;	2000EP-0301439	99US-0142055.
XX		PR	05-JUL-1999;
PR	25-FEB-1999;	99US-0121825.	99US-0142390.
PR	05-MAR-1999;	99US-0123180.	PR 08-JUL-1999;
PR	09-MAR-1999;	99US-0123548.	PR 09US-0142803.
PR	23-MAR-1999;	99US-0125788.	PR 12-JUL-1999;
PR	25-MAR-1999;	99US-0126264.	99US-0142977.
PR	29-MAR-1999;	99US-0126785.	PR 13-JUL-1999;
PR	01-APR-1999;	99US-0127462.	99US-0143542.
PR	06-APR-1999;	99US-0128234.	PR 14-JUL-1999;
PR	08-APR-1999;	99US-0128714.	99US-0143624.
PR	16-APR-1999;	99US-0129845.	PR 15-JUL-1999;
PR	19-APR-1999;	99US-0130077.	99US-0144005.
PR	21-APR-1999;	99US-0130449.	PR 16-JUL-1999;
PR	23-APR-1999;	99US-0130510.	PR 19-JUL-1999;
PR	23-APR-1999;	99US-0130891.	99US-0144332.
PR	28-APR-1999;	99US-0131449.	PR 19-JUL-1999;
PR	30-APR-1999;	99US-0132048.	99US-0144334.
PR	30-APR-1999;	99US-0132407.	PR 19-JUL-1999;
PR	04-MAY-1999;	99US-0132484.	99US-0144335.
PR	05-MAY-1999;	99US-0132485.	PR 20-JUL-1999;
PR	06-MAY-1999;	99US-0132486.	99US-0144325.
PR	06-MAY-1999;	99US-0132487.	PR 20-JUL-1999;
PR	07-MAY-1999;	99US-0132863.	99US-0144331.
PR	11-MAY-1999;	99US-0134256.	PR 21-JUL-1999;
PR	14-MAY-1999;	99US-0134256.	99US-0144332.
PR	14-MAY-1999;	99US-0134218.	PR 21-JUL-1999;
PR	14-MAY-1999;	99US-0134219.	99US-0144632.
PR	14-MAY-1999;	99US-0134221.	PR 22-JUL-1999;
PR	14-MAY-1999;	99US-0134370.	99US-0144884.
PR	18-MAY-1999;	99US-0134768.	PR 21-JUL-1999;
PR	19-MAY-1999;	99US-0134941.	99US-0145086.
PR	20-MAY-1999;	99US-0135124.	PR 19-JUL-1999;
PR	21-MAY-1999;	99US-0135353.	99US-0145088.
PR	24-MAY-1999;	99US-0135629.	PR 20-JUL-1999;
PR	25-MAY-1999;	99US-0136021.	99US-0145181.
PR	27-MAY-1999;	99US-0136392.	PR 21-JUL-1999;
PR	28-MAY-1999;	99US-0136782.	99US-0145145.
PR	01-JUN-1999;	99US-0137224.	PR 23-JUL-1999;
PR	03-JUN-1999;	99US-0137528.	99US-0145218.
PR	04-JUN-1999;	99US-0137502.	PR 22-JUL-1999;
PR	04-JUN-1999;	99US-0137502.	99US-0145224.
PR	07-JUN-1999;	99US-0137724.	PR 22-JUL-1999;
PR	08-JUN-1999;	99US-0138094.	99US-0145087.
PR	10-JUN-1999;	99US-0138540.	PR 20-JUL-1999;
PR	10-JUN-1999;	99US-0138847.	99US-0145087.
PR	14-JUN-1999;	99US-0139119.	PR 20-JUL-1999;
PR	16-JUN-1999;	99US-0139452.	99US-0145192.
PR	16-JUN-1999;	99US-0139453.	PR 21-JUL-1999;
PR	18-JUN-1999;	99US-0139458.	99US-0144884.
PR	18-JUN-1999;	99US-0139492.	PR 22-JUL-1999;
PR	18-JUN-1999;	99US-0139451.	99US-0145086.
PR	18-JUN-1999;	99US-0139461.	PR 23-AUG-1999;
PR	18-JUN-1999;	99US-0139462.	99US-0145056.
PR	18-JUN-1999;	99US-0139456.	PR 25-AUG-1999;
PR	18-JUN-1999;	99US-0139463.	99US-0145084.
PR	18-JUN-1999;	99US-0139457.	PR 26-AUG-1999;
PR	18-JUN-1999;	99US-0139750.	99US-0151065.
PR	18-JUN-1999;	99US-0139459.	PR 27-AUG-1999;
PR	18-JUN-1999;	99US-0139763.	99US-014855.
PR	21-JUN-1999;	99US-0139460.	PR 20-AUG-1999;
PR	22-JUN-1999;	99US-0139455.	99US-014902.
PR	23-JUN-1999;	99US-0139817.	PR 23-AUG-1999;
PR	23-JUN-1999;	99US-0140353.	99US-015103.
PR	24-JUN-1999;	99US-0140695.	PR 01-SEP-1999;
PR	28-JUN-1999;	99US-0140821.	PR 10-SEP-1999;
PR	29-JUN-1999;	99US-0140991.	99US-0153070.
PR	30-JUN-1999;	99US-0141287.	PR 13-SEP-1999;
PR	01-JUL-1999;	99US-0141842.	99US-0154118.
PR	16-SEP-1999;	99US-0154339.	99US-0154339.

SEQ ID NO 41.	Arabidopsis thaliana expressed polynucleotide SEQ ID NO 41.
DE	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
XX	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
KW	disease; crop; thale cress; tolerance factor; insect; pathogen; nutritive; ds.
KW	Arabidopsis thaliana.
OS	Arabidopsis thaliana.
XX	Arabidopsis thaliana.
PN	US2002023281-A1.
XX	21-FEB-2002.
XX	2001US-0770445.
XX	26-JAN-2001; 2001US-0770445.
XX	27-JAN-2000; 2000US-178472P.
XX	21-FEB-2002.
PA	(GORL/) GORLACH J.
PA	(ANY/) AN Y.
PA	(HAMI/) HAMILTON C. M.
PA	(PRIC/) PRICE J. L.
PA	(RAIN/) RAINES T. M.
PA	(YUYU/) YU Y.
PA	(RAME/) RAMEKA J. G.
PA	(PAGE/) PAGE A.
PA	(MATH/) MATHEW A. V.
PA	(LEDF/) LEDFORD B. L.
PA	(WOES/) WOESSNER J. P.
PA	(HAAS/) HAAS W. D.
PA	(GARC/) GARCIA C. A.
PA	(KRICK/) KRICKER M.
PA	(SLAT/) SLATER T.
PA	(DAVI/) DAVIS K. R.
PA	(ALLE/) ALLEN K.
PA	(HOFF/) HOFFMAN N.
PA	(HURB/) HURBAN P.
XX	Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y, Ledford BL, Woessner JP, Haas WD, Matthe AV, Slater T, Davis KR, Allen K, Hoffman N, Harban P;
WPI; 2002-400781/43.	Claim 1; SEQ ID NO 41; 49PP + Sequence Listing; English.
XX	New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein -
PT	The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN98231), given in the specification (II) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying associated physiological pathways. (I) is also useful for the genetic manipulation of cells, particularly plant cells. (I) is also useful in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress. (II) and (III) are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc., for elucidating biochemical pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening programs to identify agents that mimic or enhance the action of tolerance factors. Such agents are useful in improved methods of treating crops to enhance their tolerance to environmental stress. (I) is also useful for enhancing or inhibiting production of a biosynthetic product in a plant. (III) is useful for identifying other mediators that may induce
XX	Best Local Similarity 68.6%; Pred. No. 2.6e-18; Length 1164;
XX	Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;
Qy	1 CGACCTGCTGAAAGCAGTTGACTACCTGCTGCGAACGGCCACCACTGGTGTGGATCTGGCTCGCTGAGT 60
Db	676 CGAATGGCTTGAAGGTGACTACTTACCGCAAACTGGATCTGGTGTGGATCTGGCTCGCTGAGT 735
Db	61 C---AGCAAGCTGGCTTCCTGTAACGGAGAACTCCACCTCCGGTCTACTAGCGCG 117
Qy	736 CGAGTGTGGAGACGGATTGTGACCGGTAATCATGGATCTATGATGG 795
Db	118 CGCTCTCTGGCACCATGGAACTCCATGGCATGGCTGGCTGCAACGCGAACCCAGGT 177
Qy	796 AGGGTACTGGACAATGGAGGC-TTCCCTGTGCTGGACCCACTCGGCTCAAGTG 854
Db	178 ACAAGGAGCTGGAGGGCCATCAAACTTACCCGAACTGGCTTCCACGGGTCAATGGCT 237
Qy	805 TGAAGGAGTGGAAAGACTGGCAAGGATGCCACCCATTTAGATCATGGAT 914
Db	238 TCGACAACTTAAAGCAGAGCAGCTGGCTCAGCTTCAATAGCCCTACGGCCGG 293
Qy	915 TCGACAACTTAAAGCAGCTGGCAAGTGTCAATGGCTTCAAGCCACCAAGC 970
Db	RESULT 14 ABN98273 standard; DNA; 1205 BP. ID ABN98273 XX AC ABN98273; XX AC ABN98273; XX AC ABN98273;

CC expression of proteins of interest, for establishing the extent to which CC any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce CC tolerance to environmental stress, for identifying factors involved in biosynthetic pathways of nutritional, commercial, or medicinal value and CC for identifying products of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, CC for alteration of the cellular metabolism and for screening compounds CC that may affect the biological function of the gene or gene products.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=99990970445.

Sequence 1205 BP; 298 A; 312 C; 271 G; 322 T; 2 other;

Score 125.6; DB 24; Length 1205;

Pred. No. 2.6e-18; DR 0; Mismatches 89; Indels 4; Gaps 2;

Best Local Similarity 68.6%; Matches 203; Conservative 0; Gaps 2;

XX

Query Match 1 CGACTCTGCTGAAGCAGGTGGACTACTCTGGCGAACGGCTGGATAACCTGCCCTGCACTT

DB 671 CGAATTGGCTTAAGGAAAGTTGACTACCTTATCCGAACAGTGATTCCTGTTGATAAT 730

Qy 61 C---AGCANGTGGCTGGCTGGTGAACCGAAACTCCACCTCCGGTCTACTACAGACGG 117

Db 731 CGAGTTGGACGACGGATTGTGACCGGTAATCTGGTACCGGTAATCTACCCGATATGATG 790

Qy 118 CGCTGACTGACCATATGGTGAAGCATGCCATGTTGGCAAGGACGCCACCCAGGTG 177

Db 791 ACGGTACTGGACAAATGTGGAAAC-TTCCCCTGGTGGTGCACGGTCAAGTGT 849

Qy 178 ACAAGGAGGTGACGGACGGCATCAAATCTAACCTAACCGGACCCCTCACCGGTATCGCT 237

Db 850 TGAGGAAACTGGAGAAGATGCAAGAGGAGTACCCAAATGCCCTCATTAGATCATCGAT 909

Qy 238 TCGACAACATCAAGCAGGACGATGGTCAAGTCTACGCCCTAACAGCCCCGGGC 293

Db 910 TCGACAACATCAAGCAGGACGATGGTCAAGTCCAGTTCATAGTTICATGCCCTAACGACCCAGC 965

SQ Sequence 672 BP; 182 A; 140 C; 158 G; 192 T; 0 other;

Query Match 1 CGACCTGTAACCGAGGTGGACTACTCTGGCCAAACGGCTGGATAACCTGCCCTGCACTT

DB 469 CGATATGGCTAAAGGAGTTGACTACTCTCCGCAACAGTGGATCTCTGGTGTGAATT 410

Qy 61 C---AGCAGGAGGTGGCTGGTACCGGAGAACCTCCACCTCCGGTCTACTAGACGG 117

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Copyright (c) 1993 - 2003 Compugen Ltd.
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 (without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

• 11

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REF ID: A1120
REFERENCE 1 (bases 1 to 343)
AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

source	JOURNAL	COMMENT
1: 343 /organism="Zea mays" /mol_type="mRNA" /cultivar="W64A" /db_xref="Ucxon:4577" /tissue_type="immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli XLOR" /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose" /note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing." BASE COUNT 70 a 126 c 94 g 53 t ORIGIN	Unpublished Contact: Walbot V Department of Biological Sciences Stanford University 455 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 949026 row: D column: 10. FEATURES Source 1. .466 /organism="Zea mays" /mol_type="mRNA" /cultivar="W64A" /db_xref="taxon:4577" /tissue_type="immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli XLOR" /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose" /note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing." BASE COUNT 88 a 130 c 163 g 85 t ORIGIN	JOURNAL COMMENT Contact: Walbot V Department of Biological Sciences Stanford University 455 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 949026 row: D column: 10. FEATURES Source 1. .466 /organism="Zea mays" /mol_type="mRNA" /cultivar="W64A" /db_xref="taxon:4577" /tissue_type="immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli XLOR" /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose" /note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing." BASE COUNT 88 a 130 c 163 g 85 t ORIGIN
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RESULT 2 B1273504/c LOCUS 949026D10.x2 949 466 bp mRNA linear EST 18-JUL-2001 DEFINITION Zea mays cDNA, mRNA sequence. ACCESSION B1273504 VERSION B1273504.1 GI:14883710 KEYWORDS EST. SOURCE Zea mays ORGANISM Eukaryota; Viridiplanteae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. REFERENCE 1 (bases 1 to 466) AUTHORS Walbot,V. TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University	RESULT 3 B1245249/c LOCUS 949026D10.x1 949 471 bp mRNA linear EST 13-JUL-2001 DEFINITION Zea mays cDNA, mRNA sequence. ACCESSION B1245249 VERSION B1245249.1 GI:14717599	

KEYWORDS	Zea mays	Db	127 AGACCGGCCGCCGCCGCCGCC 105
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ORGANISM	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	RESULT 4 BG549370	BG549370	489 bp mRNA linear EST 05-APR-2001
AUTHORS	1. (bases 1 to 471) Walbot, V.	LOCUS	94704H12.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA sequence.
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University	DEFINITION	
JOURNAL	Unpublished	ACCESSION	BG549370
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu	VERSION	GI:135558014
FEATURES	Plate: 949026 row: D column: 10. Location/Qualifiers 1. .471. /organism="Zea mays" /mol_type="mRNA" /cultivar="W64A" /db_xref="taxon:4577" /tissue_type="immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli X101R" /clone_lib="N99 - Juvenile leaf and shoot cDNA from Steve Moose" /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into Lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes Yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."	source	
BASE COUNT	88 a 133 c 164 g 86 t	ORIGIN	BASE COUNT 92 a 179 c 135 g 83 t
Query Match	96.3%	Score	311; DB 12; Length 471;
Best Local Similarity	99.7%	Pred. No.	2.8e-61;
Matches	322; Conservative	0; Mismatches	0; Indels 1; Gaps 1;
Qy	1 CGACCTGGTGAACCGGTGACTACCTGGTCAAGCTGGTGTGATACCCGGCTCGAGTT	Qy	1 CGACCTGGTGAAGCAGGTGACTACCTGGTCAAGCTGGCTGATACCCGGCTCGAGTT 60
Db	426 CACCTGGTGAACCGGTGACTACCTGGTCAAGCTGGCTGATACCCGGCTCGAGTT	Db	136 CGACCTGGTGAAGCAGGTGACTACCTGGTCAAGCTGGCTGATACCCGGCTCGAGTT 195
Qy	61 CAGCAAGTGGCTTCGTTACCGGAGAACTCCACCTCCCGGTGTTACTAGAACGGCG	Qy	61 CAGCAAAGTCGCTTCGTTACCGGAGAACTCCACCTCCCGGTGTTACTAGAACGGCG 120
Db	366 CAGCAAGTGGCTTCGTTACCGGAGAACTCCACCTCCCGGTGTTACTAGAACGGCG 307	Db	196 CRGCAAAGTCGCTTCGTTACCGGAGAACTCCACCTCCCGGTGTTACTAGAACGGCG 255
Qy	121 CTACTGGACCATGCGAAGCATGCCATGTTGGCTGCAAGACGCCACCGGTGTA	Qy	121 CTACTGGACCATGCGAAGCATGCCATGTTGGCTGCAAGACGCCACCGGTGTA 180
Db	306 CTACTGGACCATGCGAAGCTGCCATGTTGGCTGCAAGACGCCACCGGTGTA	Db	256 CTACTGGACCATGCGAAGCTGCCATGTTGGCTGCAAGACGCCACCGGTGTA 314
Qy	181 AGGAGCTGGAGGCAATCAAATCTTACCCGAGCTTCAACCGGTCTATGGCTTG	Qy	181 AGGAGCTGGAGGCAATCAAATCTTACCCGAGCTTCAACCGGTCTATGGCTTG 240
Db	247 AGGAGCTGGAGGCAATCAAATCTTACCCGAGCTTCAACCGGTCTATGGCTTG	Db	315 AGGAGCTGGAGGCAATCAAATCTTACCCGAGCTTCAACCGGTCTATGGCTTG 374
Qy	241 AACACATCAAGAGCACGAGCTGGTCAAGCTGCTCATCGCTCATCGCTCATCGCT	Qy	241 AACACATCAAGAGCACGAGCTGGTCAAGCTGCTCATCGCTCATCGCTCATCGCT 300
Db	187 AACACATCAAGAGCACGAGCTGGTCAAGCTGCTCATCGCTCATCGCTCATCGCT	Db	375 AACACATCAAGAGCACGAGCTGGTCAAGCTGCTCATCGCTCATCGCTCATCGCT 128
Qy	301 AGACCGGCCGCCGCCGCCGCCGCC 323	Qy	301 AGACCGGCCGCCGCCGCCGCCGCCGCC 323

Qy 181 AGGAGCTCAGGGCCATCAAATCCCTACCGGACCCCTTCAACGGTCATGGCTCG 240
 Db 435 AGACCGGCCGCCGCCGCCGCC 457
 Qy 379 AGGAGCTCAGGGCCATCAAATCCCTACCGGACCCCTAACGGCTCATGGCTCG 438

RESULT 5

BI478737 BI478737 566 bp mRNA linear EST 27-AUG-2001
LOCUS Zea mays cDNA, mRNA sequence.
DEFINITION Zea mays cDNA, mRNA sequence.

ACCESSION BI478737
KEYWORDS EST.
SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

COMMENT 1 (bases 1 to 566)

JOURNAL Maize ESTs from various cDNA libraries sequenced at Stanford University

UNPUBLISHED

CONTACT Walbot V

DEPARTMENT Department of Biological Sciences

STANFORD UNIVERSITY 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

PLATE: 949068 **ROW**: G **COLUMN**: 08
LOCATION/QUALIFIERS
 1. .566
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W64A"
 /db_xref="taxon:4577"
 /tissue_type="immature leaf primordium and vegetative meristem"
 /dev_stage="4 stages from 3-13 days after imbibing"
 /lab_host="E. coli XLOR"
 /clone_lib="W49 - juvenile leaf and shoot cDNA from Steve Moose"
 /note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybridrap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing/imbibing in wet soil. 3. Non-green portions of developing leaves 1-5, primordia from 6-8, and portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 107 a 205 c 162 g 92 t
ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 56;
Best Local Similarity 99.7%; Pred. No. 2.9e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGACCTGCTGAACCGGGACTACTACCTGCTGCCAACGGCTGGATAACCTGGCTCGAGTT 60
Db 200 CGACCTGCTGAACCGGGACTACTACCTGCTGCCAACGGCTGGATAACCTGGCTCGAGTT 259
Qy 61 CAGCAAAGTGGCTTCGTTGCTGAGAACTCCACCTCCCGGTGCTACTAGACGCCCG 120
Db 260 CAGCAAAGTGGCTTCGTTGCTGAGAACTCCACCTCCCGGTGCTACTAGACGCCCG 319
Qy 121 CTACTGGACATCTGGAAAGCATGCCATGTTGGCTGCAACGAGCCACCCAGGTGTA 180
Db 320 CTACTGGACATCTGGAAAGCTGCCATGTTGGCTGCAACGAGCCACCCAGGTGTA 378

RESULT 6

BI396085 BI396085 578 bp mRNA linear EST 08-AUG-2001
LOCUS 940044B04.Y1 949 - Juvenile leaf and shoot cDNA from Steve Moose

DEFINITION Zea mays cDNA, mRNA sequence.

ACCESSION BI396085
VERSION BI396085.1 GI:15100294
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 578)

REFERENCE Walbot, V.

AUTHORS

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished

COMMENT Contact: Walbot V

DEPARTMENT Department of Biological Sciences

STANFORD UNIVERSITY 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

PLATE: 949044 **ROW**: B **COLUMN**: 04.

FEATURES

source Location/Qualifiers
 1. .578

source /organism="Zea mays"
 /mol_type="mRNA"
 /catalyst="W64A"
 /db_xref="taxon:4577"
 /tissue_type="immature leaf primordium and vegetative meristem"
 /dev_stage="4 stages from 3-13 days after imbibing"
 /lab_host="E. coli XLOR"
 /clone_lib="W49 - juvenile leaf and shoot cDNA from Steve Moose"
 /note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybridrap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes Yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 106 a 214 c 163 g 95 t
ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 578;
Best Local Similarity 99.7%; Pred. No. 3e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGACCTGCTGAACCGGGACTACTACCTGCTGCCAACGGCTGGATAACCTGGCTCGAGTT 60
Db 200 CGACCTGCTGAACCGGGACTACTACCTGCTGCCAACGGCTGGATAACCTGGCTCGAGTT 259
Qy 61 CAGCAAAGTGGCTTCGTTGCTGAGAACTCCACCTCCCGGTGCTACTAGACGCCCG 120
Db 260 CAGCAAAGTGGCTTCGTTGCTGAGAACTCCACCTCCCGGTGCTACTAGACGCCCG 319
Qy 121 CTACTGGACATCTGGAAAGCATGCCATGTTGGCTGCAACGAGCCACCCAGGTGTA 180
Db 320 CTACTGGACATCTGGAAAGCTGCCATGTTGGCTGCAACGAGCCACCCAGGTGTA 378

db-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACGCCAAGAAATGGGAAATTGGTTTTTTTT). The resulting DNA/RNA hybrid was treated with RNase H and used as a template for DNA PstI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pR7RT3PAC vector.

BASE COUNT 149 a 143 c 188 g 108 t

ORIGIN Query Match 96.3%; Score 311; DB 12; Length 588;
Best Local Similarity 99.7%; Pred. No. 3e-61; Gaps 1;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 517 CGACCTGTGAACCGGTGACTACCTGCTGGCAACGGCTGCTGAGTT 60
577 CGACCTGTGAACCGGTGACTACCTGCTGGCAACGGCTGCTGAGTT 518

Qy 61 CAGCAAGGTGGCTTCGTTGCGGAGAACATCCACCTCCCGTGTGTACAGCGCCG 120
Db 517 CAGCAAGGTGGCTTCGTTGCGGAGAACATCCACCTCCCGTGTGTACAGCGCCG 458

Qy 121 CTACTGGGCACATCTGGAAAGCATGCCCATGTTGGGTGCAAGCCACCCAGGTCTACA 180
Db 457 CTACTGGGCACATCTGGAAAGCATGCCCATGTTGGGTGCAAGCCACCCAGGTCTACA 399

Qy 181 AGGAGCTGAGGGGGCCTTAATCTTACCCGGACGGCTTCACCCSGCTCATGGCTTCG 240
Db 398 AGGAGCTGAGGGGGCCTTAATCTTACCCGGACGGCTTCACCCSGCTCATGGCTTCG 339

Qy 241 ACAACATAGAGAGAGGGGGCTCATGGCTTACAGGCCAGGGACT 300
Db 338 ACAACATAGAGAGAGGGGGCTCATGGCTTACAGGCCAGGGACT 279

Qy 301 AGACCGGCCGCCGCCGCC 323
Db 278 AGACCGGCCGCCGCC 256

RESULT 9
LOCUS BT1319097/c 589 bp mRNA linear EST 23-JUL-2001
DEFINITION 949039c04 .x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
Zea mays cDNA, mRNA sequence.
ACCESSION BT1319097
VERSION BT1319097.1 GI:14996976
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 589)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949039 row: C column: 04.
FEATURES Location.Qualifiers
Source 1. 589
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"

/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative meristem"
/dev_stage="4 stages from 3-13 days after imbibing"
/clone_lib="E. coli XLOR"
/lab_host="E. coli XLOR"
/note="Organ: juvenile leaf and shoot cDNA from Steve Moose"
/note="note: "PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into lambda Hybridap vector from Stratagene. Tissue Sources: 1. Whole shoot 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and growing leaves 4-5 at 13 days after sowing."
BASE COUNT 141 a 155 c 197 g
ORIGIN Query Match 96.3%; Score 311; DB 12; Length 589;
Best Local Similarity 99.7%; Pred. No. 3e-61; Gaps 1; Gaps 1;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CGACCTGTGGCTTCGTTACCTGCTGGGAAACTCCGGTGTACTACGGCTGAGTT 60
Db 502 CGACCTGTGGCTTCGTTACCTGCTGGGAAACTCCGGTGTACTACGGCTGAGTT 443
Qy 61 CAGCAAGGTGGCTTCGTTACCTGCTGGGAAACTCCGGTGTACTACGGCTGAGTT 120
Db 442 CAGCAAGGTGGCTTCGTTACCTGCTGGGAAACTCCGGTGTACTACGGCTGAGTT 383
Qy 121 CTACTGGACATGTCGAAAGCATGCCATGTTGGGTGCAAGAGCAGCCAGGGCTG 180
Db 382 CTACTGGACATGTCGAAAGCATGCCATGTTGGGTGCAAGAGCAGCCAGGGCTG 324
Qy 181 AGGAGCTGAGGGGGCTCATGGCTTACAGGCCAGGGACT 240
Db 323 AGGAGCTGAGGGGGCTCATGGCTTACAGGCCAGGGACT 264
RESULT 10
LOCUS BI430981 619 bp mRNA linear EST 17-AUG-2001
DEFINITION 949039c09.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
Zea mays cDNA, mRNA sequence.
ACCESSION BI430981
VERSION BI430981.1 GI:15209097
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 619)
AUTHORS Walbot V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
COMMENT Unpublished
JOURNAL Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Plate: 949039 row: C column: 04.
FEATURES Location.Qualifiers
Source 1. 589
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"

855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 949063 row: F column: 09.
 Location/Qualifiers
 1..619
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="W64A"
 /db_xref="taxon:4577"
 /tissue_type="immature leaf primordium and vegetative
 meristem"
 /dev_stage="4 stages from 3-13 days after imbibing"
 /lab_host="E. coli XLOR"
 /clone_id="949 - juvenile leaf and shoot cDNA from Steve
 Moose"
 /note="Organ: juvenile vegetative shoots; Vector:
 pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XbaI; Equal amounts
 of total RNA by weight from 4 tissue sources (see below)
 were pooled, polyA+ RNA isolated, and cDNA synthesized for
 EcoRI (S') and XbaI (3') direction cloning into Lambda
 Hybrid vector from Stratagene. Tissue Sources: 1. Whole
 shoots 3 days after sowing/imbibing in wet soil. 2. Basal
 1.5 cm shoots 6 days after sowing - includes yellow
 portions of developing leaves 1-5, primordia from 6-8, and
 the vegetative apex. 3. Non-green portions of developing
 leaves 4-5 and the vegetative apex, including adult leaf
 primordia, 9 days after sowing. 4. Partially expanded and
 greening leaves 4-5 at 13 days after sowing."
 BASE COUNT
 ORIGIN
 110 a 225 c 177 g 107 t
 Query Match 96.3%; Score 311; DB 12; Length 619;
 Best Local Similarity 99.7%; Pred. No. 3e-61;
 Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 CGACCTGCTGAAAGCAGTGGACTACCTGTGGCAACGGCTGGATAACCCCTGCAGTT 60
 Db 208 CGACCTGCTGAAAGCAGTGGACTACCTGTGGCAACGGCTGGATAACCCCTGCAGTT 267
 Qy 61 CAGCAAGGTGGCTTCCTGTACCGGAGAACCTCACCTCCGGTGTACATAGCGGCCG 120
 Db 268 CAGCAGGTGGCTTCCTGTACCGGAGAACCTCACCTCCGGTGTACATAGCGGCCG 327
 Qy 121 CTACTGGACATGTGGAGCATGCCATTGGCTGCAAGGCAACCCAGGTCTACA 180
 Db 328 CTACTGGACATGTGGAGCTTGCCATTGGCTGCAAGGCAACCCAGGTCTACA 386
 Qy 181 AGGAGCTGCAAGGAGGCCATCAAATCTTACCGGAGCCCTTCACCCGGTCTACGGCTTCG 240
 Db 387 ACCAGCTGCAAGGAGGCCATCAAATCTTACCGGAGCCCTTCACCCGGTCTACGGCTTCG 446
 Qy 241 ACAACTCAAGAGGCCATGGCTGCTAGCTTACATCGCTAACAGGCCGGCAGGACT 300
 Db 447 ACAACTCAAGAGGCCATGGCTGCTAGCTTACATCGCTAACAGGCCGGCAGGACT 506
 Qy 301 AGACCGGCCGCCGCCGCCGCC 323
 Db 507 AGACCGGCCGCCGCCGCC 529
 BASE COUNT
 ORIGIN
 117 a 224 c 172 g 109 t
 Query Match 96.3%; Score 311; DB 10; Length 622;
 Best Local Similarity 99.7%; Pred. No. 3e-61;
 Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 CGACCTGCTGAAAGCAGTGGACTACCTGTGGCAACGGCTGGATAACCCCTGCAGTT 60
 Db 244 CGACCTGCTGAAAGCAGTGGACTACCTGTGGCAACGGCTGGATAACCCCTGCAGTT 303
 Qy 61 CAGCAAGGTGGCTTCCTGTACCGGAGAACCTCACCTCCGGTGTACATAGCGGCCG 120
 Db 304 CAGCAGGTGGCTTCCTGTACCGGAGAACCTCACCTCCGGTGTACATAGCGGCCG 363
 Qy 121 CTACTGGACATGTGGAGCATGCCATTGGCTGCAAGGCAACCCAGGTCTACA 180
 Db 364 CTACTGGACATGTGGAGCTTGCCATTGGCTGCAAGGCAACCCAGGTCTACA 422
 Qy 181 AGGAGCTGCAAGGAGGCCATCAAATCTTACCGGAGCCCTTCACCCGGTCTACGGCTTCG 240
 Db 423 AGGAGCTGCAAGGAGGCCATCAAATCTTACCGGAGCCCTTCACCCGGTCTACGGCTTCG 482
 Qy 241 ACAACTCAAGAGGCCATGGCTGCTAGCTTACATCGCTAACAGGCCGGCAGGACT 300
 Db 483 ACAACTCAAGAGGCCATGGCTGCTAGCTTACATCGCTAACAGGCCGGCAGGACT 542
 Qy 301 AGACCGGCCGCCGCCGCCGCC 323
 Db 543 AGACCGGCCGCCGCCGCCGCC 565
 RESULT 11
 BG458523 Locus BG458523 622 bp mRNA linear EST 19-MAR-2001
 Definition 947045B08.Y1 947 - 2 week shoot from Barkan lab Zea mays cdNA, mRNA
 Sequence
 Accession BG458523
 Version BG458523.1 GI:13381848
 Source EST
 Keywords Zea mays
 Organism Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 622)
 REFERENCE
 AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 Unpublished
 JOURNAL Contact: Walbot V
 COMMENT Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 947045 row: B column: 08.
 Location/Qualifiers
 1..622
 /organism="Zea mays"
 /mol_type="mRNA"
 /culFivarc="B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf and stem, including leaf base"
 /dev_stage="2 week old seedling (3 leaves)"
 /lab_host="XII-Blue"
 /clone_lib="947 - 2 week shoot from Barkan lab"
 /note="Organ: shoot; Vector: Lambda ZAP (pBluescript SK+);
 Site 1: EcoRI; Site 2: XbaI; Directionally cloned using
 Stratagene's UniZap XR cDNA cloning kit with the 5' end
 at the EcoRI site. The library represents 8 x 10^5
 independent recombinant phage. The plants were greenhouse
 grown."
 BASE COUNT
 ORIGIN
 117 a 224 c 172 g 109 t
 RESULT 12
 AW352495 Locus AW352495 652 bp mRNA linear EST 02-FEB-2000
 Definition 707050B11.Y1 707 - Mixed adult tissues from Walbot lab (SK) Zea
 mays CDNA, mRNA sequence.
 Accession AW52495
 Version AW52495.1 GI:6881485
 Source EST
 Keywords Zea mays
 Organism Zea mays

RESULT 14	Db	296	AGGACCTGCAGGGCCATCAATCCATTACCCGGCTTCCACCGGTCAAGCCGCTCATCGCTTC	237	
LOCUS	BI319103	475	bp	mRNA	
DEFINITION	949039D04 x2 949 - Juvenile leaf and shoot cDNA from Steve Moose	linear	EST 23-JUL-2001		
ACCESSION	Qy	241	ACAACATCAGAGGAGCTGCTGAGCTCATCGCTCAAGCCCGGAGGACT	300	
VERSION	Db	236	ACAACATCAGAGGAGCTGCTGAGCTCATCGCTCAAGCCCGGAGGACT	177	
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Embryophyta; Poales; Poaceae; PACCAD	RESULT 15			
AUTHORS	1 (bases 1 to 475)	LOCUS	BR055905	553 bp	
TITLE	Waibot,V.	DEFINITION	945017B1_1.Y1 945 - Mixed adult tissues from Walbot lab, same as 707	mRNA linear EST 08-JUN-2000	
JOURNAL	Maine ESTs from various cDNA libraries sequenced at Stanford University	ACCESSION	BB055905	mRNA sequence.	
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 94039 row: D column: 04.	VERSION	BB055905.1	GI: 8382962	
FEATURES	Location/Qualifiers	KEYWORDS	Zea mays		
Source	1. .475	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Liliopsida; Poales; Poaceae; Andropogoneae; Zea.		
Source	/organism="Zea mays"	ORGANISM	Zea mays		
Source	/mol_type="mRNA"	CULTIVAR	"W23"		
Source	/cultivar="W64A"	/db_xref="taxon:4577"			
Source	/db_xref="E. coli XIOLR"	TISSUE	type="tassel, kernel, silk, husk, root, leaf"		
Source	/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"	DEV_STAGE	"fully-grown"		
Source	/dev_stage="4 stages from 3-13 days after imbibing"	LAB_HOST	"DH10B"		
Source	/lab_host="E. coli XIOLR"	CLONE_ID	"945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"		
Source	/clone_id="949 - Juvenile leaf and shoot cDNA from Steve Moose"	NOTE	/note="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-1.1, Site 1: EcoRI, Site 2: XbaI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated and cDNA synthesized for EcoRI (5') and XbaI (3') directional cloning into Lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."		
BASE COUNT	110 a 123 c 164 g 78 t	ORIGIN	given to library 707 for additional sequencing."		
ORIGIN	101 a 197 c 157 g 98 t	BASE COUNT	101	ORIGIN	
Query Match	95.8%	Score	309.4;	DB 10;	
Best Local Similarity	99.4%	Pred. No.	6.6e-61;	Length 553;	
Matches	321;	Conservative	0;	Mismatches 1;	
Qy	1	GACACTGCTGAGCACTGGACTACCTGCTGCCAACGGCTGATCGACTT	60	Query Match 95.8%; Score 309.4; DB 10; Length 553; Best Local Similarity 99.4%; Pred. No. 6.6e-61; Mismatches 1;	
Db	475	GACACTGCTGAGCACTGGACTACCTGCTGCCAACGGCTGATCGACTT	416	Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
Qy	61	GAGCAAGGTGCCCTTGCTGAGCACTGGACTACCTGCCGTGACTAGCGCCG	120	Qy 1 CGACCTGCTGAAGCTGGGACTACCTGCTGCCAACGGCTGATCGACTT	60
Db	415	CAGCAAGGTGCCCTTGCTGAGCACTGGACTACCTGCCGTGACTAGCGCCG	356	61 CAGCAAGGTGCCCTTGCTGAGCACTGGACTACCTGCTGCCAACGGCTGATCGACTT	120
Qy	121	CTACTGGACCATGTGGAAAGCTGCCATGTCGGCTGCCAACGGCTGATCGACT	180	Db 138 CGACCTGCTGAAGCTGGACTACCTGCCGTGACTAGCGCCG	257
Db	355	CTACTGGACCATGTGGAAAGCTGCCATGTCGGCTGCCAACGGCTGATCGACT	297	Qy 121 CTACTGGACCATGTGGAAAGCTGCCATGTCGGCTGCCAACGGCTGATCGACT	180
Qy	258	GGAGCTGCAAGGCAATCCATGTCGGCTGCCAACGGCTGATCGACT	240	Db 181 CTACTGGACCATGTGGAAAGCTGCCATGTCGGCTGCCAACGGCTGATCGACT	316

Qy	181	AGGAGCTGCAGGGGCCATCAAATCCTACCGGACCCCTTCCACCGCGTCAATCGGCTTG	240
	317	ACGAGCTGCAGGGCCATCAAATCCTACCGGACCCCTTCCACCGCGTCAATCGGCTTG	376
Db			
Qy	241	ACAACATCAAGCAGACCGAGGCGCTAGCTCATGGCTTACAGCTTCATGGCTTACAAAGCCCCGGCAGCGACT	300
Db	377	ACAACATCAAGCAGACCCAGTGTCTAGCTTCATGGCTTACAAAGCCCCGGCAGCGACT	436
Qy	301	AGACCCGGCCCGGGCC 323	
Db	437	AGACCCGGCCCGGGCC 459	

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